

OM protein - protein search, using sw model

Run on: January 7, 2004, 20:04:17 ; Search time 37.848 Seconds

(without alignments) 4223.507 Million cell updates/sec

Title: US-10-014-269-34

Sequence: 5279

1 MGEEGSGASDEHERASVTL.....LKINNCITYLGAALLQAP 1007

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_19Jun03.*
1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT*
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT*
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT*
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT*
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8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT*
9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT*
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15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT*
16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT*
17: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1996.DAT*
18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT*
19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT*
20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT*
21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT*
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5279	100.0	1007	23	AAE25434 Human Nod2 mutant.
2	5279	100.0	1007	23	ABJ04766 Nod2a protein del
3	5272	99.9	1038	23	ABJ04735 Nod2a protein wild
4	5272	99.9	1040	23	AAE25416 Human Nod2 protein
5	5271	99.8	1007	23	ABJ04767 Nod2a P2685 + Iram
6	5271	99.8	1040	23	ABJ04773 Nod2a V9531 protei
7	5268	99.8	1040	23	ABJ04771 Nod2a V793K protei
8	5268	99.8	1040	23	ABJ04774 Nod2a M863V protei
9	5267	99.8	1040	23	AAE25418 Human Nod2 sequen
10	5267	99.8	1040	23	ABJ04737 Nod2 protein sequ
11	5267	99.8	1040	23	ABJ04772 Nod2a R202W protei
12	5264	99.7	1040	23	ABJ04769 Nod2a G208R (SNP17
13	5264	99.7	1040	23	ABJ04770 Nod2a P2685 + N852
14	5264	99.7	1040	23	ABJ04776 Nod2a P2685 + G980
15	5259	99.6	1040	23	ABJ04775 Nod2a P2685 + R702
16	5256	99.6	1040	23	AAE25417 Amino acid sequenc
17	5256	99.6	1040	23	AAE25419 Human Nod2 protein
18	5155	97.7	1041	22	AAE25417 Human Nod2 protein
19	5128	97.1	1013	23	ABJ04736 Nod2a protein wild
20	5128	97.1	1013	23	ABJ04736 Nod2a protein wild
21	4935.5	93.5	1009	23	AAU80865 Human CARD3X prote
22	4188	79.3	795	23	AAU80875 Human CARD3X prote
23	2859	56.1	560	23	AAU80856 Human CARD3X prote
24	2887	39.5	403	23	AAU80870 Human CARD3X prote
25	1614	30.6	305	23	AAE25421 Human CARD3X prote
26	1614	30.6	305	23	ABJ04740 Human CARD3X prote
27	1564	29.6	286	23	AAU80869 Human CARD3X prote
28	1175.5	22.3	953	20	AAE20064 Murine CARD-4L (lon
29	1175.5	22.3	953	22	ABJ31145 Mouse caspase recr
30	1175.5	22.3	953	23	ABG31080 Protein of murine
31	1175.5	22.3	953	23	AAO22136 Mouse Caspase recr
32	1175.5	22.3	953	24	ABU56298 Human protein SEQ
33	1173	22.2	953	21	AAE15532 Apoptosis related
34	1170.5	22.2	953	22	AAV74473 Human Caspase recr
35	1170.5	22.2	953	22	AAV74489 Human Caspase recr
36	1170.5	22.2	953	22	AAE20080 Human CARD-4L (lon
37	1170.5	22.2	953	23	AAO22111 Human Caspase recr
38	1169.5	22.2	953	24	ABU56273 Human Caspase recr
39	1169.5	22.2	953	23	ABG31076 Human CARD-4L prot
40	1165.5	22.1	953	20	AAV31141 Caspase recruitmen
41	1132	21.4	966	24	ABU56300 Apoptosis related
42	962	18.2	705	21	AAE15559 Fragment of apopto
43	962	18.2	705	21	ABJ15562 Human colon cancer
44	962	18.2	719	22	AAE75589 Human protein sequ
45	887.5	16.8	779	22	AAE95610

Search completed: January 7, 2004, 20:49:55
Job time : 41.848 secs

OM protein - protein search, using sw model

Run on: January 7, 2004, 20:54:33 ; Search time 29.6176 Seconds

(without alignments)
6851.332 Million cell updates/sec

Title: US-10-014-269-34

Perfect score: 5279
Sequence: 1 MGEEGGSASHDEERASVLT.....LKTNNCTVIGAEMLQAP 1007

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747907 seqs, 201509753 residues

Total number of hits satisfying chosen parameters: 747907

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA.*
1: /cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubppaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubppaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubppaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubppaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubppaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubppaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubppaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubppaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubppaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubppaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubppaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubppaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	ID	Description
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Search completed: January 7, 2004, 21:06:03
Job time : 32.6176 secs

1	5279	100.0	1007	12	US-10-314-506-34	Sequence 34, Appl
2	5279	100.0	1007	14	US-10-014-269-34	Sequence 34, Appl
3	5279	100.0	1007	14	US-10-002-974-34	Sequence 34, Appl
4	5272	99.9	1040	12	US-10-314-506-2	Sequence 2, Appl
5	5272	99.9	1040	14	US-10-014-269-2	Sequence 2, Appl
6	5272	99.9	1040	14	US-10-002-974-55	Sequence 55, Appl
7	5271	99.8	1007	12	US-10-314-506-55	Sequence 55, Appl
8	5271	99.8	1007	14	US-10-002-974-55	Sequence 55, Appl
9	5271	99.8	1040	14	US-10-002-974-63	Sequence 63, Appl
10	5269	99.8	1040	14	US-10-002-974-63	Sequence 63, Appl
11	5268	99.8	1040	12	US-10-002-974-63	Sequence 63, Appl
12	5267	99.8	1040	14	US-10-314-506-4	Sequence 4, Appl
13	5267	99.8	1040	14	US-10-002-974-4	Sequence 4, Appl
14	5267	99.8	1040	14	US-10-002-974-65	Sequence 65, Appl
15	5264	99.7	1040	12	US-10-314-506-57	Sequence 57, Appl
16	5264	99.7	1040	14	US-10-002-974-57	Sequence 57, Appl
17	5264	99.7	1040	14	US-10-002-974-59	Sequence 59, Appl
18	5264	99.7	1040	14	US-10-002-974-61	Sequence 61, Appl
19	5259	99.6	1040	14	US-10-002-974-61	Sequence 61, Appl
20	5256	99.6	1040	12	US-10-314-506-59	Sequence 59, Appl
21	5256	99.6	1040	12	US-10-314-506-61	Sequence 61, Appl
22	5256	99.6	1040	14	US-10-002-974-85	Sequence 85, Appl
23	5256	99.6	1040	14	US-10-002-974-85	Sequence 85, Appl
24	5256	99.6	1040	14	US-10-002-974-89	Sequence 89, Appl
25	5155	97.7	1041	12	US-10-240-046A-2	Sequence 2, Appl
26	5128	97.1	1013	12	US-10-314-506-3	Sequence 3, Appl
27	5128	97.1	1013	14	US-10-014-269-3	Sequence 3, Appl
28	5128	97.1	1013	14	US-10-002-974-3	Sequence 3, Appl
29	4935.5	93.5	1009	10	US-09-864-921-107	Sequence 107, App
30	4188	79.3	795	10	US-09-864-921-188	Sequence 188, App
31	2959	56.1	560	10	US-09-864-921-83	Sequence 83, Appl
32	2087	39.5	403	10	US-09-864-921-176	Sequence 176, App
33	1614	30.6	305	12	US-10-314-506-7	Sequence 7, Appl
34	1614	30.6	305	14	US-10-014-269-7	Sequence 7, Appl
35	1614	30.6	305	14	US-10-002-974-7	Sequence 7, Appl
36	1864	29.6	296	10	US-09-864-921-174	Sequence 174, App
37	1175.5	22.3	953	9	US-09-728-721-43	Sequence 43, Appl
38	1175.5	22.3	953	14	US-10-118-984-43	Sequence 43, Appl
39	1175.5	22.3	953	15	US-10-295-981-43	Sequence 43, Appl
40	1170.5	22.2	953	9	US-09-728-721-8	Sequence 8, Appl
41	1170.5	22.2	953	12	US-10-028-374-4	Sequence 4, Appl
42	1170.5	22.2	953	12	US-10-183-770-4	Sequence 4, Appl
43	1170.5	22.2	953	14	US-10-105-931-8	Sequence 8, Appl
44	1170.5	22.2	953	14	US-10-118-984-8	Sequence 8, Appl
45	1170.5	22.2	953	15	US-10-013-477-12	Sequence 12, Appl

OM protein - protein search, using sw model

Run on: January 7, 2004, 20:49:58 ; Search time 16.7833 Seconds
(without alignments)
5770.121 Million cell updates/sec

Title: US-10-014-269-34

Perfect score: 5279

Sequence: 1 MEIEGSGASHDEERASVLT.....LKLNNCITYLGAFLIAP 1007

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 76:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Match	Length	DB	ID	Description
1	404	7.7	1130	2	A48843		MHC class II trans
2	390	7.4	1152	2	T17235		hypothetical prote
3	350.5	6.6	1111	2	A59000		matern protein (imp
4	232.5	4.4	456	2	A31857		ribonuclease inh
5	227	4.3	461	2	A31858		ribonuclease-angio
6	213	4.0	506	2	A45841		T-complex-associat
7	210	4.0	456	2	S20597		ribonuclease inh
8	210	4.0	535	2	T48102		RAN GTPase activat
9	210	4.0	1075	2	T31668		hypothetical prote
10	207.5	3.9	631	2	C89243		protein F28C1.3 (i
11	207.5	3.9	631	2	T21471		hypothetical prote
12	207	3.9	1004	2	T31665		hypothetical prote
13	206	3.9	533	2	T52063		ran GTPase-activat

14	197	3.7	789	2	T52067		hypothetical prote
15	191.5	3.6	1010	2	T36383		probable large ATP
16	190.5	3.6	545	2	T52068		RAN GTPase-activat
17	185.5	3.5	1447	2	T42628		neuronal apoptosis
18	184.5	3.5	483	2	S27880		Nasopressin recept
19	173.5	3.3	862	2	T36380		probable large ATP
20	158	3.0	1232	2	A53478		neuronal apoptosis
21	156	3.0	332	2	T52069		GTPase-activating
22	154	2.9	1119	2	AB2239		hypothetical prote
23	150.5	2.9	312	2	B97746		hypothetical prote
24	150.5	2.9	1096	2	A96607		protein disease re
25	146	2.8	1411	2	S44770		C29E4.3 protein -
26	145	2.7	998	2	T23427		hypothetical prote
27	144.5	2.7	861	2	T36381		hypothetical prote
28	143.5	2.7	567	2	U55300		probable large ATP
29	140	2.7	1121	2	T02764		RAN GTPase activat
30	133	2.5	589	2	T52070		myosin-I binding p
31	130	2.5	618	2	T48193		RNAl protein homol
32	128	2.4	589	2	A36883		hypothetical prote
33	127.5	2.4	603	2	U66128		RNAl homolog fugu
34	126.5	2.4	1347	2	A12043		insulin-like growt
35	125.5	2.4	1256	2	AB2042		hypothetical prote
36	124	2.3	1151	2	T30936		reverse transcript
37	122	2.3	183	2	F97803		hypothetical prote
38	121.5	2.3	386	2	S37691		hypothetical prote
39	121	2.3	518	2	D96512		ran GTPase activat
40	121	2.3	800	2	AB1129		hypothetical prote
41	120.5	2.3	849	2	C97303		interleukin A (limp
42	120	2.3	662	2	S42799		hypothetical prote
43	120	2.3	1091	2	A58532		garp precursor - h
44	119.5	2.3	680	2	T19939		glial cell membran
45	119.5	2.3	808	2	B97303		hypothetical prote

Search completed: January 7, 2004, 20:53:39
Job time : 18.7833 secs

OM protein - protein search, using sw model

Run on: January 7, 2004, 20:05:32 ; Search time 11.1899 Seconds

(without alignments)
4232,403 Million cell updates/sec

Title: US-10-014-269-34

Perfect score: 5279

Sequence: 1 MGEEGGASASDEBERASVLT.....LKLNNCITYLGKALQAP 1007

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5272	99.9	1040	1	CARF_HUMAN
2	4070	77.1	1020	1	CARF_MOUSE
3	1178.5	22.3	953	1	CARD_MOUSE
4	1170.5	22.2	953	1	CARD_MOUSE
5	511	9.7	1062	1	PRAT_HUMAN
6	488.5	9.3	1033	1	CISI_MOUSE
7	486.5	9.2	1034	1	CISI_MOUSE
8	417.5	7.9	1155	1	C2TA_MOUSE
9	404	7.7	1130	1	C2TA_HUMAN
10	390	7.4	1473	1	NAL1_HUMAN
11	385.5	7.3	854	1	PYAS_MOUSE
12	374.5	7.1	980	1	PYAS_MOUSE
13	374	7.1	994	1	NAL1_HUMAN
14	372	7.0	1062	1	NAL1_HUMAN
15	361.5	6.8	892	1	PYAS_MOUSE
16	360.5	6.8	843	1	PYAS_MOUSE
17	350.5	6.6	1111	1	MATE_MOUSE

18	335	6.3	1200	1	MATE_HUMAN	P59047 homo sapien
19	292	5.5	1033	1	PYAS_HUMAN	P59045 homo sapien
20	232.5	4.4	456	1	RINI_PIG	P10775 sus scrofa
21	227	4.3	460	1	RINI_HUMAN	P13469 homo sapien
22	223	4.2	1403	1	BIR1_MOUSE	Q9j1b6 mus musculus
23	221.5	4.2	1024	1	CARF_HUMAN	Q9np44 homo sapien
24	214.5	4.1	1402	1	BIR1_MOUSE	Q9j1b3 mus musculus
25	210	4.0	456	1	RINI_PIG	P29315 ratus norv
26	206.5	3.9	1403	1	BIR1_MOUSE	Q9p4k5 mus musculus
27	185.5	3.5	1447	1	BIR1_MOUSE	Q9p4k5 mus musculus
28	185	3.5	1403	1	BIR1_MOUSE	Q9p4k5 mus musculus
29	157.5	3.0	1403	1	BIR1_MOUSE	Q9p4k5 mus musculus
30	157.5	3.0	1403	1	BIR1_MOUSE	Q9p4k5 mus musculus
31	154.5	2.9	350	1	REP1_MOUSE	Q13073 homo sapien
32	146	2.8	1411	1	YK63_MOUSE	Q13066 xenopus lae
33	143.5	2.7	587	1	REP1_HUMAN	P34342 cecropia
34	128	2.4	589	1	REP1_MOUSE	P46060 homo sapien
35	127.5	2.4	603	1	ALS_MOUSE	P46061 mus musculus
36	121.5	2.3	386	1	RNAI_MOUSE	P70389 mus musculus
37	121	2.3	800	1	RNAI_MOUSE	P41391 schizosach
38	120	2.3	662	1	RNAI_MOUSE	P25146 listeria mo
39	117.5	2.2	1037	1	CARF_HUMAN	Q14392 homo sapien
40	114.5	2.2	4128	1	PRKD_MOUSE	Q9p4k6 homo sapien
41	113.5	2.2	2594	1	7LES_MOUSE	P97313 mus musculus
42	113	2.1	359	1	TMO1_HUMAN	P20806 drosophila
43	112	2.1	603	1	ALS_MOUSE	P23289 homo sapien
44	112	2.1	820	1	TRE1_MOUSE	P35859 ratus norv
45	111	2.1	356	1	P622_MOUSE	P54910 agrobacteri

ALIGNMENTS

RESULT 1	ID	Query Match	Length	DB ID	Description
CARF_HUMAN	AC	Q9HC29, Q96RH5, Q96RH6, Q96RH8	1040 AA.		
CARF_HUMAN	DT	28-FEB-2003 (Rel. 41, Created)			
CARF_HUMAN	DT	28-FEB-2003 (Rel. 41, Last sequence update)			
CARF_HUMAN	DT	15-SEP-2003 (Rel. 42, Last annotation update)			
CARF_HUMAN	DE	Caspase recruitment domain protein 15 (Nod2 protein) (Inflammatory)			
CARF_HUMAN	DE	boxel disease protein 11.			
CARF_HUMAN	GN	CARD15 OR NOD2 OR IBD1.			
CARF_HUMAN	GN	Home sapiens (Human).			
CARF_HUMAN	OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
CARF_HUMAN	OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
CARF_HUMAN	OX	NCBI_TaxID=9606;			
CARF_HUMAN	RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), MLAGENESIS OF LYS-305, AND			
CARF_HUMAN	RP	VARIANT ARG-908.			
CARF_HUMAN	RP	TISSUE=Brain;			
CARF_HUMAN	RP	PUBMED=11087742;			
CARF_HUMAN	RA	Ogura Y., Inohara N., Benito A., Chen F.F., Yamoka S., Nunez G.,			
CARF_HUMAN	RT	"Nod2, a Nod1/Apa1 family member that is restricted to monocytes and			
CARF_HUMAN	RT	activates NF-kappaB";			
CARF_HUMAN	RT	J Biol. Chem. 276:4612-4618 (2001).			
CARF_HUMAN	RT	[2]			

RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), VARIANTS CD THR-140, ARG-157;
RP CYS-235, ARG-248, SER-268, SER-289, ASN-291, VAL-301, TRP-311;
RP VAL-348, ARG-352, CYS-373, SER-418, LEU-431, VAL-432, LYS-441;
RP VAL-612, THR-612, TRP-684, TRP-702, CYS-703, CYS-713, GLY-725;
RP VAL-755, VAL-758, LYS-778, MET-793, LYS-843, SER-853, VAL-863;
RP ARG-908, ASP-918, ASP-924 AND ILE-955, VARIANTS ULCERATIVE COLITIS
RP THR-140 AND THR-885, AND VARIANT MET-189.
RC TISSUE=leukocyte;
RX MEDLINE=21279172; PubMed=1186576;
RA Hugot J.-P., Chamailhard M., Zouali H., Lesage S., Gerard J.-P.,
RA Belacene J., Almer S., Tyak C., O'Morain C.A., Gassull M., Binder V.,
RA Finkel Y., Cortot A., Modigliani R., Laurent-Pug P.,
RA Gower-Rousseau C., Macry J., Colombel J.-F., Sabaout M., Thomas G.,
RT "Association of NOD2 leucine-rich repeat variants with susceptibility
RT to Crohn's disease.";
RL Nature 411:599-603(2001).
RN [3].
RP VARIANTS BS GLN-334, TRP-334 AND PHE-469.
RX MEDLINE=21419644; PubMed=11528384;
RA McCell-Richard C., Lesage S., Rybojad M., Prieur A.M.,
RA Manouvrier-Hanu S., Harter R., Chamailhard M., Zouali H., Thomas G.,
RA Hugot J.-P.,
RT "CARD15 mutations in Blau syndrome.";
RL Nat. Genet. 29:19-20(2001).
CC -|- FUNCTION: Induces NF-kappaB via RICK (CARDIAC, RIP2) and IKK-
CC gamma. Confers responsiveness to intracellular bacterial
CC 1, lipopolysaccharides (LPS).
CC -|- SUBUNIT: Binds to RICK by CARD-CARD interaction.
CC -|- SUBCELLULAR LOCATION: Cytoplasmic.
CC -|- ALTERNATIVE PRODUCTS:
CC Event=Alternative initiation;
CC Comment=2 isoforms, 1/Nod2 (shown here) and 2/Nod2b are
CC produced by alternative initiation. Both isoforms can activate
CC NF-kappaB. Isoform 1 is more abundant.
CC -|- TISSUE SPECIFICITY: Monocytes-specific.
CC -|- DISEASE: Defects in CARD15 are the cause of Blau syndrome (BS)
CC [MIM:186580], a rare autosomal dominant disorder characterized by
CC early-onset granulomatous arthritis, uveitis and skin rash.
CC -|- DISEASE: Defects in CARD15 are a cause of susceptibility to
CC Crohn's disease (CD) [MIM:266600], a form of remitting
CC inflammatory bowel disease. CD may involve any part of the
CC gastrointestinal tract, but most frequently the terminal ileum and
CC colon. Bowel inflammation is transmural and discontinuous. Crohn's
CC disease is commonly classified as autoimmune disease.
CC -|- DISEASE: Defects in CARD15 are a cause of susceptibility to
CC ulcerative colitis [MIM:191390], a chronic inflammatory bowel
CC disease. In ulcerative colitis, the inflammation is continuous and
CC limited to rectal and colonic mucosal layers. Ulcerative colitis
CC is commonly classified as autoimmune disease.
CC -|- SIMILARITY: Contains 2 CARD domains.
CC -|- SIMILARITY: Contains 1 NACHT domain.
CC -|- SIMILARITY: Contains 6 leucine-rich (LRR) repeats.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC DR PROSITE; PSS0209; CARD; 2.
CC DR PROSITE; PSS0837; NACHT; 1.
CC KW AIP-binding; Repeat; Leucine-rich repeat; Disease mutation;
CC KW Alternative initiation; Polymorphism.
CC CHAIN 1 1040
CC FT
CC FT CHAIN 28 1040
CC FT
CC FT INIT_MET 28 28
CC FT DOMAIN 26 122
CC FT DOMAIN 126 218
CC FT DOMAIN 293 618
CC FT NP_BIND 299 306
CC FT REPEAT 786 812
CC FT REPEAT 814 837
CC FT REPEAT 842 865
CC FT REPEAT 926 949
CC FT REPEAT 954 977
CC FT REPEAT 982 1005
CC FT VARIANT 140 140
CC FT
CC FT VARIANT 157 157
CC FT
CC FT VARIANT 189 189
CC FT
CC FT VARIANT 235 235
CC FT
CC FT VARIANT 248 248
CC FT
CC FT VARIANT 268 268
CC FT
CC FT VARIANT 289 289
CC FT
CC FT VARIANT 291 291
CC FT
CC FT VARIANT 294 294
CC FT
CC FT VARIANT 301 301

CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC DR EMBL: AF178930; AAC33677.1; -
CC DR EMBL: AF385089; AAK70867.1; -
CC DR EMBL: AF385090; AAK70868.1; -
CC DR EMBL: AJ303140; CAC42117.1; -
CC DR Genem; HGNC:5331; CARD15.
CC DR MIM: 605956; -
CC DR MIM: 186580; -
CC DR MIM: 266600; -
CC DR MIM: 191390; -
CC DR InterPro; IPR001315; CARD.
CC DR InterPro; IPR001611; LRR.
CC DR InterPro; IPR007091; LRR_N1inh.
CC DR InterPro; IPR007111; NACHT_NTPase.
CC DR Pfam; PF00560; LRR; 2.
CC DR SMART; SMO011

FT	VARIANT	311	311	/FtId=VAR_012674. R-> W (in CD and ulcerative colitis).	FT	VARIANT	924	924	G-> D (in CD).
FT	VARIANT	334	334	/FtId=VAR_012675. R-> Q (in BS).	FT	VARIANT	955	955	/FtId=VAR_012703. V-> L.
FT	VARIANT	334	334	/FtId=VAR_012676. R-> W (in BS).	FT	MUTAGEN	305	305	/FtId=VAR_012704. K->R: NO ACTIVATION.
FT	VARIANT	348	348	/FtId=VAR_012677. L-> V (in CD).	SEQ	SEQUENCE	1040 AA:	115282 MW; 003759295607DDEFCRC64;	
FT	VARIANT	352	352	/FtId=VAR_012678. H-> R (in CD).	Query Match				
FT	VARIANT	373	373	/FtId=VAR_012679. R-> C (in CD).	Best Local Similarity 100.0%; Pred. No. 0;				
FT	VARIANT	414	414	/FtId=VAR_012680. N-> S (in CD).	Matches 1006; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
FT	VARIANT	431	431	/FtId=VAR_012681. S-> L (in CD).	QY	1	MEEGGSAHDEERASVLLGHSFGCCSCGQAQAQSQVLLVSGSLIEGFSTLDM	60	
FT	VARIANT	432	432	/FtId=VAR_012682. A-> V (in CD).	DB	1	MEEGGSAHDEERASVLLGHSFGCCSCGQAQAQSQVLLVSGSLIEGFSTLDM	60	
FT	VARIANT	441	441	/FtId=VAR_012683. E-> K (in CD).	QY	61	LSWEVLSWEDYEGFHLLGQPLSHLARLLDITVWKGTWACOKLTAAGQEAQSQSPKLL	120	
FT	VARIANT	469	469	/FtId=VAR_012684. L-> F (in BS).	DB	61	LSWEVLSWEDYEGFHLLGQPLSHLARLLDITVWKGTWACOKLTAAGQEAQSQSPKLL	120	
FT	VARIANT	612	612	/FtId=VAR_012685. A-> T (in CD).	QY	121	GGMPSHLPRADQSHRAIYRRLSHVENKDLAMERGYSQYECDEIRLPIFTSQR	180	
FT	VARIANT	612	612	/FtId=VAR_012686. A-> V (in CD).	DB	121	GGMPSHLPRADQSHRAIYRRLSHVENKDLAMERGYSQYECDEIRLPIFTSQR	180	
FT	VARIANT	684	684	/FtId=VAR_012687. R-> W (in CD).	DB	181	ARRLLDIATVKAAGIAFLIQHQLPEVPLPLEAATCKRYMAKLTYSAGSRFLSTY	240	
FT	VARIANT	702	702	/FtId=VAR_012688. R-> W (risk factor for CD).	QY	181	ARRLLDIATVKAAGIAFLIQHQLPEVPLPLEAATCKRYMAKLTYSAGSRFLSTY	240	
FT	VARIANT	703	703	/FtId=VAR_012689. R-> C (in CD and ulcerative colitis).	DB	181	ARRLLDIATVKAAGIAFLIQHQLPEVPLPLEAATCKRYMAKLTYSAGSRFLSTY	240	
FT	VARIANT	713	713	/FtId=VAR_012690. R-> C (in CD).	QY	241	DGATLGLDITVNVLEVWADYGAAPQKSPATLQLEELFTPGHLDNDADIVLVGE	300	
FT	VARIANT	725	725	/FtId=VAR_012691. A-> G (in CD).	DB	241	DGATLGLDITVNVLEVWADYGAAPQKSPATLQLEELFTPGHLDNDADIVLVGE	300	
FT	VARIANT	735	735	/FtId=VAR_012692. A-> V (in CD and ulcerative colitis).	QY	301	AGSGKSTLLQRLHLLMAAQDQDEFLTFEPFSCQQLQCAKPLSVTLTFEHCCMPDVQ	360	
FT	VARIANT	758	758	/FtId=VAR_012693. A-> V (in CD).	DB	301	AGSGKSTLLQRLHLLMAAQDQDEFLTFEPFSCQQLQCAKPLSVTLTFEHCCMPDVQ	360	
FT	VARIANT	778	778	/FtId=VAR_012694. E-> K (in CD).	QY	361	EDIFQLDLHPRYVLLTFDGFDEKRFETDRRCSPDPSTVQTLFLNLQGLLNAR	420	
FT	VARIANT	793	793	/FtId=VAR_012695. V-> M (in CD).	DB	361	EDIFQLDLHPRYVLLTFDGFDEKRFETDRRCSPDPSTVQTLFLNLQGLLNAR	420	
FT	VARIANT	843	843	/FtId=VAR_012696. E-> K (in CD).	QY	421	KVTSRPAASAFKRYITRENLKGSZDQGELEYLKRHHFGVADRLRLDETSAH	480	
FT	VARIANT	853	853	/FtId=VAR_012697. N-> S (in CD).	DB	421	KVTSRPAASAFKRYITRENLKGSZDQGELEYLKRHHFGVADRLRLDETSAH	480	
FT	VARIANT	863	863	/FtId=VAR_012698. M-> V (in CD).	QY	481	GLCHLPFSMWSKHOELLLOEGGSKITTMKYLILLCHFLHRTPPSASQGLSPSL	540	
FT	VARIANT	885	885	/FtId=VAR_012699. A-> T (in ulcerative colitis).	DB	481	GLCHLPFSMWSKHOELLLOEGGSKITTMKYLILLCHFLHRTPPSASQGLSPSL	540	
FT	VARIANT	908	908	/FtId=VAR_012700. G-> R (in CD).	QY	541	RGRPLTLHGRLLAMGLAMCCYVFSNQLQAQVSPDLSIGFLYAKGVPSSTAPLE	600	
FT	VARIANT	918	918	/FtId=VAR_012701. A-> D (risk factor for CD).	DB	541	RGRPLTLHGRLLAMGLAMCCYVFSNQLQAQVSPDLSIGFLYAKGVPSSTAPLE	600	
FT	VARIANT			/FtId=VAR_012702.	QY	601	FLHTFCCFAAFYALSDVPPALHLHFNCGRGSPARLLPTKCIQASEGSDSVA	660	
					DB	601	FLHTFCCFAAFYALSDVPPALHLHFNCGRGSPARLLPTKCIQASEGSDSVA	660	
					QY	661	ALLQKAPENLQITAFLLAGLLSRHGGLLACQTSKALRQACRMCLARSIRGHR	720	

Db 661 ALIQKAPPHUQITAFIAGLSREHWGLAEQYSEKALLRQACRQCLASLRKFFH 720
 QY 721 SIPPAPGSAKSVHAMPGEIWLISLVKEQEEELARPAAGLNVGHKLIFCSVGPTECA 780
 Db 722 SIPPAPGSAKSVHAMPGEIWLISLVKEQEEELARPAAGLNVGHKLIFCSVGPTECA 780
 QY 781 ALAFVQLHRRVVALQIDNVSVDIGVEQLPCGVCKLYLRDNNISDRGICKILECAL 840
 Db 782 ALAFVQLHRRVVALQIDNVSVDIGVEQLPCGVCKLYLRDNNISDRGICKILECAL 840
 QY 841 HCEQLQMLALFNNKLTIDGCAHSMKALLACRQNFALRLANNYITAGAQVLAEGIRGTS 900
 Db 842 HCEQLQMLALFNNKLTIDGCAHSMKALLACRQNFALRLANNYITAGAQVLAEGIRGTS 900
 QY 901 LQFLGFWGNRVGDEGAQALAEALGDHQSILRWLSLVGNNTGSVGAQALATMLARVMLEEL 960
 Db 902 LQFLGFWGNRVGDEGAQALAEALGDHQSILRWLSLVGNNTGSVGAQALATMLARVMLEEL 960
 QY 961 CLEENHLQDEGVCSLAEGIKRNSLSKILKLSNNCITYLGAELLQA 1006
 Db 962 CLEENHLQDEGVCSLAEGIKRNSLSKILKLSNNCITYLGAELLQA 1006

Search completed: January 7, 2004, 20:50:47
 Job time : 16.1889 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 7, 2004, 20:45:37 ; Search time 33.5667 Seconds

(without alignments)
7741.578 Million cell updates/sec

Title: US-10-014-269-34

Perfect score: 5279
Sequence: 1 WGEQGSAASHDEERASVLL.....LKLNNCITYLGAELLQAP 1007

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: SP archaea:*
- 2: SP bacteria:*
- 3: SP fungi:*
- 4: SP human:*
- 5: SP invertebrate:*
- 6: SP mammal:*
- 7: SP mhc:*
- 8: SP organelle:*
- 9: SP phage:*
- 10: SP plant:*
- 11: SP rodent:*
- 12: SP virus:*
- 13: SP vertebrate:*
- 14: SP unclassified:*
- 15: SP virus:*
- 16: SP bacteriaph:*
- 17: SP archaeap:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Score	Match	Length	DB	ID	Description
No.							

1	4070	77.1	1020	11	Q8K3Z0	Q8K3Z0 mus musculus
2	1178.5	22.3	953	11	Q8B8B0	Q8B8B0 mus musculus
3	1170.5	22.2	953	4	Q8IWF5	Q8IWF5 homo sapien
4	975	18.5	706	11	Q8BUL6	Q8BUL6 mus musculus
5	489.5	9.3	1033	11	Q8R4B8	Q8R4B8 mus musculus
6	479.5	9.1	892	4	Q8NEU4	Q8NEU4 homo sapien
7	419.5	7.9	1153	7	Q8CJEC	Q8CJEC rattus norv
8	417.5	7.9	1155	7	Q8RPPI	Q8RPPI mus musculus
9	405.5	7.7	778	4	Q8WFA8	Q8WFA8 homo sapien
10	395.5	7.5	1052	7	Q8CUD8	Q8CUD8 rattus norv
11	393.5	7.5	1073	7	Q8CUD9	Q8CUD9 rattus norv
12	377.5	7.2	713	6	Q8S1Z7	Q8S1Z7 macaca fasc
13	357.5	6.8	733	4	Q8TEE2	Q8TEE2 homo sapien
14	354.5	6.7	982	11	Q8BU40	Q8BU40 mus musculus
15	339.5	6.4	1056	4	Q8NFA2	Q8NFA2 homo sapien
16	332	6.3	846	4	Q8IXT0	Q8IXT0 homo sapien
17	328	6.2	499	4	Q8TEL3	Q8TEL3 homo sapien
18	321	6.1	692	4	Q8EDS1	Q8EDS1 homo sapien
19	316.5	6.0	660	4	Q8NFO6	Q8NFO6 homo sapien
20	302	5.7	863	11	Q8C6J9	Q8C6J9 mus musculus
21	297	5.6	884	7	Q29675	Q29675 homo sapien
22	297	5.6	932	4	Q86KL4	Q86KL4 homo sapien
23	296.5	5.6	977	7	Q8HW99	Q8HW99 mus musculus
24	288	5.5	1097	4	Q8H6Y0	Q8H6Y0 mus musculus
25	282	5.3	312	11	Q8BY65	Q8BY65 mus musculus
26	282	5.3	397	11	Q8BUFA	Q8BUFA mus musculus
27	268	5.1	603	10	Q83ZV8	Q83ZV8 arabidopsi
28	262	5.0	195	4	Q8NI01	Q8NI01 homo sapien
29	262	5.0	223	4	Q8NI02	Q8NI02 homo sapien
30	248	4.7	748	11	Q89WU0	Q89WU0 mus musculus
31	242.5	4.6	620	16	Q8XZN9	Q8XZN9 talstonia s
32	236	4.5	554	4	Q8H7Z4	Q8H7Z4 mus musculus
33	234.5	4.4	519	11	Q8C249	Q8C249 mus musculus
34	232.5	4.4	825	11	Q8CEM5	Q8CEM5 mus musculus
35	228	4.3	461	4	Q8IZK8	Q8IZK8 homo sapien
36	227	4.3	447	4	Q8FEF7	Q8FEF7 homo sapien
37	227	4.3	461	6	Q8HZP9	Q8HZP9 pan troglod
38	227	4.3	817	5	Q864V6	Q864V6 dictyostell
39	226.5	4.3	673	11	Q8CCN1	Q8CCN1 mus musculus
40	226	4.3	461	4	Q8BQ80	Q8BQ80 homo sapien
41	226	4.3	753	4	Q869L7	Q869L7 homo sapien
42	225	4.3	681	10	Q8YIX2	Q8YIX2 arabidopsi
43	223	4.2	1403	11	Q8CH64	Q8CH64 mus musculus
44	222	4.2	1403	11	Q8CH68	Q8CH68 mus musculus
45	216.5	4.1	1787	10	Q8Y4X9	Q8Y4X9 chlamydomon

Search completed: January 7, 2004, 20:52:41
 Job time : 38.5667 secs

OM nucleic - protein search, using frame_plus_nbp model

Run on: January 7, 2004, 19:23:16 ; Search time 110.762 Seconds
(without alignments)
12857.211 Million cell updates/sec

Title: US-10-014-269-33
Perfect score: 8270
Sequence: 1 gtagcagatccagcagctcac.....ataacitcttgagtaaac 4486

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1107863 seqs, 158726573 residues
Total number of hits satisfying chosen parameters: 2215726

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Command line parameters:

-MODEL=frame+_nbp.model -DEV=xlp
Q=/cm2_1/USPTO_spool_P/US10014269/runat_07012004_175228_24497/app_query.fasta_1
.9358
-DB=A_Geneseq_19Jun03 -OFMT=fastan -SUFFIX=tag -MINMATCH=0.1 -IOPCCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blsum62 -TRANS=human40.cdi
-LIST=150 -DOCALLIGN=200 -THR_SCORE=pcpt -THR_MAX=100 -THR_MIN=0 -ALIGN=50
-MODE=LOCAL -OUTFMT=pcp -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10014269 @CGN 1 1 311 @runat_07012004_175228_24497 -NCPU=6 -ICPU=3
-NO MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPLOCK=100 -LONLOC
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
-Fgapext=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

A_Geneseq_19Jun03:.*
1: /SIDSI/gcdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDSI/gcdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDSI/gcdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDSI/gcdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDSI/gcdata/geneseq/geneseq-emb1/AA1984.DAT.*
6: /SIDSI/gcdata/geneseq/geneseq-emb1/AA1985.DAT.*
7: /SIDSI/gcdata/geneseq/geneseq-emb1/AA1986.DAT.*
8: /SIDSI/gcdata/geneseq/geneseq-emb1/AA1987.DAT.*
9: /SIDSI/gcdata/geneseq/geneseq-emb1/AA1988.DAT.*
10: /SIDSI/gcdata/geneseq/geneseq-emb1/AA1989.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	DB ID	Description
1	5435	65.7	1040 23	AAE25416 Human Nod2 protein
2	5434	65.7	1040 23	ABJ04773 Nod2a V935I protei
3	5432	65.7	1040 23	ABJ04771 Nod2a V935V protei
4	5431	65.7	1040 23	ABJ04774 Nod2a M663V protei
5	5430	65.7	1040 23	AAE25418 Human Nod2 protein
6	5430	65.7	1040 23	ABJ04737 Nod2 protein sequ
7	5430	65.7	1040 23	ABJ04772 Nod2a N855S protei
8	5427	65.6	1038 23	ABJ04735 Nod2a protein wild
9	5427	65.6	1040 23	ABJ04768 Nod2a R702W protei
10	5427	65.6	1040 23	ABJ04769 Nod2a P268S + N852
11	5422	65.6	1040 23	ABJ04770 Nod2a P268S + N852
12	5422	65.6	1040 23	ABJ04775 Nod2a P268S + R702
13	5419	65.5	1040 23	ABJ04777 Amino acid sequen
14	5419	65.5	1040 23	ABJ04772 Human Nod2 protein
15	5318	64.3	1041 22	AAE25417 Human Nod2 protein
16	5291	64.0	1013 23	ABJ04736 Human Nod2 protein
17	5279	63.8	1007 23	AAE25434 Human Nod2 mutant.
18	5279	63.8	1007 23	ABJ04766 Nod2a protein delt
19	5271	63.7	1007 23	ABJ04767 Human Nod2a P268S + fram
20	5271	63.7	1009 23	AAU80865 Human CARD3X prote
21	4981.5	60.2	1009 23	AAU80865 Human CARD3X prote
22	4188	50.6	795 23	AAU80875 Human CARD3X prote
23	2959	35.8	560 23	AAU80876 Human CARD3X prote
24	2087	25.2	403 23	AAU80870 Human CARD3X prote
25	1614	19.5	305 23	AAE25421 Human Nod2 protein
26	1614	19.5	305 23	ABJ04740 Nod2 nucleotide bi
27	1564	18.9	296 23	AAU80869 Human CARD3X NB-AR
28	1206.5	14.6	953 20	AAV31145 Murine CARD3X-4L pro
29	1206.5	14.6	953 22	ABG31080 Mouse CARD-4L (lon
30	1206.5	14.6	953 23	AAO22136 Mouse caspase recr
31	1206.5	14.6	953 23	AAO22136 Protein of murine
32	1206.5	14.6	953 24	ABU36258 Mouse Caspase recr
33	1199	14.5	959 22	AAV79473 Human protein SEQ

34	1196.5	14.5	953	21	AAH15552	Apoptosis related
35	1196.5	14.5	953	22	AAH78489	Human protein S50
36	1196.5	14.5	953	22	AAH20080	Human CARD-4L (lon
37	1196.5	14.5	953	23	AAO22111	Protein of human C
38	1196.5	14.5	953	23	AAH56273	Human Caspase recr
39	1195.5	14.5	953	23	AAH31076	Human caspase recr
40	1191.5	14.4	953	20	AAH31141	Human CARD-4L prot
41	1158	14.0	966	24	AAH56300	Caspase recruitment
42	998	11.9	705	21	AAH15559	Apoptosis related
43	998	11.9	705	21	AAH15562	Fragment of apopto
44	998	11.9	719	22	AAH75589	Human colon cancer
45	887.5	10.7	779	22	AAH5610	Human protein sequ
46	858	10.4	166	22	AAH49110	Human liver peptid
47	858	10.4	166	22	AAH29107	Peptide #1758 enco
48	858	10.4	166	22	AAH51062	Protein #1701 enco
49	858	10.4	166	22	AAH67453	Human bone marrow
50	858	10.4	166	22	AAH30324	Peptide #1706 enco
51	858	10.4	166	22	AAH30704	Human peptide enco
52	858	10.2	155	22	AAH38892	Human liver peptid
53	840	10.2	155	22	AAH43475	Peptide #10981 enc
54	840	10.2	155	22	AAH64339	Protein #6438 enco
55	840	10.2	155	22	AAH64407	Human brain expres
56	840	10.2	155	22	AAH7225	Human bone marrow
57	840	10.2	155	22	AAH21157	Peptide #7591 enco
58	840	10.2	155	22	AAH21368	Peptide #11405 enc
59	840	10.2	155	22	AAH6236	Human peptide enco
60	820	9.9	146	22	AAH68853	Human liver peptid
61	820	9.9	146	22	AAH3476	Peptide #10982 enc
62	820	9.9	146	22	AAH6440	Protein #913 enco
63	820	9.9	146	22	AAH77226	Human brain expres
64	820	9.9	146	22	AAH77226	Human bone marrow
65	820	9.9	146	22	AAH21158	Peptide #7592 enco
66	820	9.9	146	22	AAH7369	Peptide #11406 enc
67	820	9.9	146	22	AAH6237	Human peptide enco
68	820	9.9	146	22	AAH80876	Human CARD3X prote
69	639.5	7.7	180	23	AAH80877	Mouse CARD3X #1.
70	593	7.2	140	23	AAH80877	Mouse CARD3X #2.
71	588	7.1	139	23	AAH31142	Human CARD-45 (sho
72	530.5	6.4	490	20	AAH31142	Human CARD-45 (sho
73	530.5	6.4	490	22	AAH31142	Human CARD-45 (sho
74	530.5	6.4	490	23	AAH31142	Human CARD-45 (sho
75	530.5	6.4	490	23	AAH31142	Human CARD-45 (sho
76	530.5	6.4	490	23	AAH31142	Human CARD-45 (sho
77	522	6.3	97	23	AAH31142	Human CARD-45 (sho
78	522	6.3	97	23	AAH31142	Human CARD-45 (sho
79	521.5	6.3	1061	23	AAH31142	Human CARD-45 (sho
80	521.5	6.3	1061	23	AAH31142	Human CARD-45 (sho
81	494.5	6.0	1034	22	AAH31142	Human CARD-45 (sho
82	494.5	6.0	1034	22	AAH31142	Human CARD-45 (sho
83	485	5.9	94	23	AAH31142	Human CARD-45 (sho
84	485	5.9	94	23	AAH31142	Human CARD-45 (sho
85	439	5.3	975	22	AAH31142	Human CARD-45 (sho
86	438.5	5.3	19938	24	AAH31142	Human CARD-45 (sho
87	430	5.2	967	19	AAH31142	Human CARD-45 (sho
88	430	5.2	1207	19	AAH31142	Human CARD-45 (sho
89	429	5.2	1106	19	AAH31142	Human CARD-45 (sho
90	429	5.2	1130	16	AAH31142	Human CARD-45 (sho

148 342.5 4.1 1200 24 AAE31749
 149 342 4.1 1111 24 AAE31748
 150 341.3 4.1 777 14 AAE31740

Human WATER protei
 Mouse WATER protei
 Collagen-like poly

Search completed: January 7, 2004, 19:42:16
 Job time : 379.762 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model .
 Run on: January 7, 2004, 19:49:02 ; Search time 134.015 Seconds
 (without alignments)
 13490.627 Million cell updates/sec

Title: US-10-014-269-33
 Perfect score: 8270
 Sequence: 1 gtagacagatccaggtctcac.....ataaacgttgatgaataaac 4486

Scoring table: BLOSUM62
 Xgapop 10.0 , Xgapext 0.5
 Ygapop 10.0 , Ygapext 0.5
 Fgapop 6.0 , Fgapext 7.0
 Delop 6.0 , Delext 7.0

Searched: 747907 seqs, 201509793 residues

Total number of hits satisfying chosen parameters: 1495814

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 150 summaries

Command line parameters:

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 .9358
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 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
 -TRANS=human40.cdi -LIST=150 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100
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 -LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
 -Fgapop=6 -Fgapext=7 -Ygapop=10 -Ygapext=0.5 -Delop=6 -Delext=7

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpa/PTC_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpa/PTCUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpa/US09_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpa/US09B_PUBCOMB.pep:*

97	407	4.9	1429	12	US-10-183-770-15	Sequence 15, Appl
98	407	4.9	1429	15	US-10-028-392-11	Sequence 11, Appl
99	407	4.9	1454	10	US-09-388-221-10	Sequence 10, Appl
100	407	4.9	1473	10	US-09-388-221-2	Sequence 2, Appl
101	393.5	4.8	919	12	US-10-094-749-2718	Sequence 2718, Ap
102	392	4.7	858	9	US-09-848-035-8	Sequence 8, Appl
103	392	4.7	858	10	US-09-866-224-8	Sequence 8, Appl
104	392	4.7	994	11	US-09-965-621-16	Sequence 16, Appl
105	392	4.7	994	12	US-10-407-866-16	Sequence 16, Appl
106	392	4.7	994	15	US-10-066-521-24	Sequence 24, Appl
107	384.5	4.6	952	12	US-10-407-866-70	Sequence 70, Appl
108	382.5	4.6	1033	12	US-10-132-967-2	Sequence 2, Appl
109	382.5	4.6	1033	14	US-10-127-516-2	Sequence 2, Appl
110	382.5	4.6	1033	14	US-10-027-629-2	Sequence 2, Appl
111	382	4.6	1062	12	US-10-239-663-43	Sequence 43, Appl
112	379.5	4.6	1049	12	US-10-239-663-42	Sequence 42, Appl
113	379	4.6	635	12	US-10-407-866-90	Sequence 90, Appl
114	378.5	4.6	772	12	US-10-094-749-2366	Sequence 13, Appl
115	374.5	4.5	980	9	US-09-848-035-13	Sequence 13, Appl
116	374.5	4.5	980	10	US-09-965-621-13	Sequence 13, Appl
117	363.5	4.4	947	11	US-09-965-621-18	Sequence 18, Appl
118	363.5	4.4	947	12	US-10-407-866-18	Sequence 18, Appl
119	362	4.4	902	12	US-10-407-866-66	Sequence 66, Appl
120	357	4.3	1111	15	US-10-216-645-5	Sequence 5, Appl
121	352.5	4.3	674	12	US-10-407-866-89	Sequence 89, Appl
122	352.5	4.3	719	11	US-09-965-621-59	Sequence 59, Appl
123	352.5	4.3	719	12	US-10-407-866-59	Sequence 59, Appl
124	351	4.2	1344	15	US-10-066-521-6	Sequence 6, Appl
125	350	4.2	612	12	US-10-407-866-88	Sequence 88, Appl
126	344	4.2	1143	15	US-10-216-645-4	Sequence 4, Appl
127	344	4.2	1162	15	US-10-216-645-2	Sequence 2, Appl
128	341.5	4.1	720	12	US-10-342-331-4	Sequence 4, Appl
129	339.5	4.1	635	12	US-10-296-539-2	Sequence 2, Appl
130	339.5	4.1	635	12	US-10-407-866-84	Sequence 84, Appl
131	339.5	4.1	635	15	US-10-066-521-13	Sequence 13, Appl
132	339	4.1	590	12	US-10-407-866-94	Sequence 94, Appl
133	338	4.1	1466	12	US-10-301-822-33	Sequence 33, Appl
c 134	338	4.1	1466	15	US-10-177-293-68	Sequence 68, Appl
c 135	336.5	4.1	720	12	US-10-342-331-4	Sequence 4, Appl
136	331	4.0	584	12	US-10-029-866-32446	Sequence 32446, A
137	329.5	4.0	821	9	US-09-848-035-2	Sequence 2, Appl
138	329.5	4.0	821	10	US-09-965-621-2	Sequence 2, Appl
139	329	4.0	200	9	US-09-728-721-11	Sequence 11, Appl
140	329	4.0	200	14	US-10-105-931-11	Sequence 11, Appl
141	329	4.0	200	15	US-10-118-984-11	Sequence 11, Appl
142	329	4.0	200	15	US-10-285-981-11	Sequence 21, Appl
c 143	328.5	4.0	1078	15	US-10-058-124-21	Sequence 116, Appl
c 144	328.5	4.0	960	12	US-10-342-331-5	Sequence 91, Appl
145	323.5	3.9	321	12	US-10-407-866-116	Sequence 116, Appl
146	321.5	3.9	659	12	US-10-407-866-91	Sequence 91, Appl
147	316	3.8	875	9	US-09-848-035-16	Sequence 16, Appl
148	316	3.8	875	10	US-09-965-621-16	Sequence 16, Appl
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Search completed: January 7, 2004, 20:34:10
Job time : 430.015 secs

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OM nucleic - protein search, using frame_plus_n2p model
Run on: January 7, 2004, 19:24:31 / Search time 65.5073 seconds
(without alignments)
13171.439 Million cell updates/sec

Title: US-10-014-269-33
Perfect score: 8270
Sequence: 1 gtagacagatccaggtccac.....ataactgttgatcaaac 4486

Scoring table:
BLOSUM62
Xgapop 10.0 / Xgapext 0.5
Ygapop 10.0 / Ygapext 0.5
Fgapop 6.0 / Fgapext 7.0
Delop 6.0 / Delext 7.0

Searched: 283308 seqs, 96168682 residues
Total number of hits satisfying chosen parameters: 56616
Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Command line parameters:
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-UNITS=bits -START=1 -END=1 -MATRIX=blomsu62 -TRANS=human40.cdf -LIST=150
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-OUTFMT=prf -NOM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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Database :
1: PIR_76:*
2: PIR:*
3: PIR:*
4: PIR:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
SUMMARIES

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1	429	5.2	1130	2	A48843	MGC class II trans
2	390	4.7	1192	2	T17255	hypothetical prote
3	357	4.3	1111	2	A59000	major protein (imp
4	338	4.1	1466	1	CGHU7L	collagen alpha 1(I
5	329.5	4.0	1453	2	S21626	collagen alpha 1(I
6	322.5	3.9	2944	2	A54849	collagen alpha 1(V
7	315.5	3.8	1496	1	CGHU2V	collagen alpha 2(V
8	312.5	3.8	1464	2	S59856	collagen alpha 1(I
9	312	3.8	784	2	JQ0317	hypothetical 82K p
10	310.5	3.8	1464	1	CGHU1L	collagen alpha 1(I
11	310.5	3.8	1466	1	CGHU7L	collagen alpha 1(I
12	310	3.8	1464	2	S59856	collagen alpha 1(I
13	309	3.8	1373	1	A43291	collagen alpha 2(I
14	308.5	3.8	660	1	Q08B3	BHLF1 protein - hu
15	305	3.7	1049	1	CGH07S	collagen alpha 1(I
16	301.5	3.7	1487	1	CGHU6C	collagen alpha 1(I
17	301.5	3.6	1691	1	S22917	collagen alpha 5(I
18	297.5	3.6	1670	1	CGHU3B	collagen alpha 3(I
19	294.5	3.6	1049	1	CGH07S	collagen alpha 1(I
20	294.5	3.6	1418	2	T45467	collagen alpha 1(I
21	294	3.6	779	1	CGH01S	collagen alpha 1(I
22	291	3.5	1414	1	S23809	collagen alpha 1(I
23	289.5	3.5	2715	2	T13049	collagen alpha 2(I
24	288.5	3.5	1497	2	I49607	eyelid - fruit fly
25	288.5	3.5	1466	1	CGHU2E	procollagen type V
26	287.5	3.5	1366	1	CGHU2S	collagen alpha 2(I
27	287	3.5	886	2	I50694	collagen alpha 1(I
28	287	3.5	886	2	I50694	collagen alpha 1(I
29	287	3.5	886	2	I50694	collagen alpha 1(I
30	286.5	3.5	1690	1	CGHU1S	collagen alpha 4(I
31	284	3.5	671	1	CGHRTS	collagen alpha 4(I
32	283.5	3.5	1487	2	B41182	collagen alpha 1(I
33	283.5	3.4	2944	2	A54849	collagen alpha 1(V
34	282.5	3.4	1806	1	CGHU1E	collagen alpha 1(X
35	281	3.4	1414	1	S23809	collagen alpha 2(I
36	280	3.4	1638	1	CGHU9V	collagen alpha 1(I
37	276.5	3.4	1119	2	A41182	collagen alpha 1(I
38	275.5	3.4	1042	1	CGCH1S	collagen alpha 1(I
39	273.5	3.3	1453	2	S21626	collagen alpha 1(I
40	269.5	3.3	1418	2	T45467	collagen alpha 1(I
41	269	3.3	1464	1	CGHU1S	collagen alpha 1(I
42	268.5	3.3	1603	1	S23810	collagen alpha 1(X
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45	268	3.2	1487	2	B41182	collagen alpha 1(I
46	268	3.2	1843	2	S18903	collagen alpha 1(V
47	266	3.2	1691	2	S22917	collagen alpha 5(I
48	264	3.2	1591	2	T31611	hypothetical prote
49	264	3.2	1669	1	CGHU4B	collagen alpha 1(I
50	263.5	3.2	1496	1	CGHU2V	collagen alpha 2(V
51	263.5	3.2	1806	1	CGHU1E	collagen alpha 1(X
52	263	3.2	1669	1	CGH54B	collagen alpha 1(X
53	262.5	3.2	1492	2	A40333	collagen alpha 1(I
54	261.5	3.2	1487	1	CGHU6C	collagen alpha 1(I
55	259	3.1	779	1	CGH01S	collagen alpha 1(I
56	258.5	3.1	1763	2	S16366	collagen alpha 2(I
57	258	3.1	486	2	A31657	ribonuclease inhib
58	257.5	3.1	2715	2	T13049	eyelid - fruit fly
59	257	3.1	1373	1	A43291	collagen alpha 2(I
60	256.5	3.1	1838	1	CGHU1V	collagen alpha 1(V
61	255.5	3.1	888	2	S28791	collagen alpha 1(X
62	255.5	3.1	1492	2	A40333	collagen alpha 1(V
63	255.5	3.1	1492	2	A40333	collagen alpha 1(V
64	254.5	3.1	1670	1	CGHU2E	collagen alpha 2(V
65	254.5	3.1	1543	1	CGHU3B	collagen alpha 3(I
66	253	3.1	1843	2	S18903	collagen alpha 1(X
67	252	3.0	1586	1	CGHU2S	collagen alpha 2(I
68	252	3.1	1486	1	B40333	BHLF1 protein - hu
69	250	3.0	1486	1	B40333	collagen alpha 1(I
70	249.5	3.0	1758	2	T29350	collagen alpha 1(I
71	249.5	3.0	1759	2	T29351	hypothetical prote
72	247	3.0	1344	1	A35175	collagen alpha 2(I
73	246.5	3.0	920	2	B34493	mucln I precursor,
74	246.5	3.0	1603	2	S23810	collagen alpha 1(I
75	245.5	2.9	1357	2	T29265	collagen alpha 1(X
76	243.5	2.9	1497	2	I49607	hypothetical prote
77	243.5	3.0	1549	2	I48103	procollagen type V
78	241.5	2.9	1712	1	CGHU2B	type VII collagen
79	241.5	2.9	1763	2	S16366	collagen alpha 2(I
80	241	2.9	744	1	A34246	collagen alpha 2(I
81	240.5	2.9	964	1	S23298	collagen alpha 1(V
82	240	2.9	13288	1	CGCH2S	collagen alpha 1(V
83	239.5	2.9	920	2	A45748	mucln, submaxillar
84	239.5	2.9	1549	2	I48103	collagen alpha 1(V
85	239.5	2.9	1549	2	I48103	type VII collagen
86	239	2.9	1460	1	EDBEIF	collagen alpha 1(I
87	239	2.9	1707	2	A33526	immediate-early pr
88	238.5	2.9	627	2	A44112	collagen alpha 2(I
89	238	2.9	1758	2	T23350	spidron 2, dregil
90	238	2.9	1758	2	T23351	hypothetical prote
91	238	2.9	1759	2	T23351	collagen alpha 2(I
92	238	2.9	1791	2	T02345	hypothetical prote
93	237	2.9	1428	2	T08852	lustrin A - Calfo
94	236.5	2.9	1066	2	JQ0405	hypothetical 119.5
95	235	2.8	1707	2	A33526	collagen alpha 2(I
96	234.5	2.8	931	2	S13580	collagen alpha 1(I
97	234.5	2.8	4857	2	T03455	collagen alpha 1(I
98	234	2.8	5262	2	T03454	collagen alpha 1(I
99	233.5	2.8	1691	1	CGHU5B	collagen alpha 6(I
100	232.5	2.8	1106	2	JQ0405	collagen alpha 1(I
101	231.5	2.8	506	2	A45841	hypothetical 119.5
102	231	2.8	754	2	A55267	7-complex-associated
103	231	2.8	920	2	A45748	collagen alpha 5(I
104	229.5	2.8	1585	2	T31611	collagen alpha 1(V
105	229.5	2.8	1585	2	A45748	collagen alpha 1(V
106	228	2.8	825	2	A43426	hypothetical prote
107	228	2.8	1446	1	A45344	collagen alpha 2 f
108	227.5	2.8	461	2	A31858	DNA-binding protei
109	226	2.7	1360	2	T33922	immediate-early pr
110	225.5	2.7	2142	2	B35098	ribonuclease-endo
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c 112	225	2.7	1669	1	CGH048	collagen alpha 1(I
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c 114	223.5	2.7	1027	2	S28774	collagen alpha cha
c 115	223.5	2.7	1574	2	T13954	MEGF6 protein - ra
c 116	223	2.7	1024	2	S18251	collagen alpha 1(X
c 117	222.5	2.7	1446	1	A45344	immediate-early pr
c 118	222	2.7	671	1	CGRT15	collagen alpha 1(I
c 119	222	2.7	1774	2	B6101	collagen alpha 1(X
c 120	222	2.7	4957	2	T03455	ALR protein - huma
c 121	222	2.7	5262	2	T03454	ALR protein - huma
c 122	221.5	2.7	964	1	CGCH25	collagen alpha 2(I
c 123	221.5	2.7	2321	2	S78549	notch3 protein - h
c 124	220.5	2.7	1315	2	A56101	collagen alpha 1(X
c 125	219.5	2.7	1712	1	CGH028	collagen alpha 2(I
c 126	219	2.6	456	2	S20587	ribonuclease inh
c 127	219	2.7	1752	2	A45407	collagen alpha 3(I
c 128	218.5	2.6	2232	2	T34344	hypothetical prote
c 129	218	2.6	677	2	S23286	collagen alpha 2(I
c 130	218	2.6	744	2	S15435	collagen alpha 1(V
c 131	218	2.7	1870	2	S37671	MHC class III hist
c 132	217.5	2.6	1184	2	G01763	atrophin-1 - huma
c 133	217.5	2.7	1872	2	S36152	MHC class III hist
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c 135	215.5	2.6	743	1	S23779	collagen alpha 1(V
c 136	215.5	2.6	921	2	S42617	collagen alpha 1(I
c 137	215.5	2.6	1532	2	A61262	collagen alpha 1(X
c 138	215	2.6	635	2	A57131	collagen alpha 2(V
c 139	214.5	2.6	635	2	A57131	collagen alpha 2(V
c 140	214.5	2.6	1574	2	T13954	MEGF6 protein - ra
c 141	214	2.6	1691	1	CGH058	collagen alpha 6(I
c 142	213.5	2.6	920	2	B34493	collagen alpha 1(I
c 143	213	2.6	931	2	S13580	collagen alpha 1(I
c 144	213	2.6	1460	1	EDBE1F	immediate-early pr
c 145	212.5	2.6	2796	2	JC4743	fatty-acid synthas
c 146	212	2.6	825	1	EDBE1D	immediate-early pr
c 147	211.5	2.6	1964	2	T09059	notch4 - mouse
c 148	211	2.5	730	2	A36226	collagen alpha 1 c
c 149	210.5	2.5	1027	2	S28774	collagen alpha cha
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Search completed: January 7, 2004, 19:34:38
Job time : 511.507 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: January 7, 2004, 19:24:01 ; Search time 34.7539 Seconds
(without alignments)
12140.333 Million cell updates/sec

Title: US-10-014-269-33
Percent score: 8270
Sequence: 1 gtgacagatccagctcac.....ataactgttgatcaaac 4486

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 127863 seqs, 47026705 residues
Total number of hits satisfying chosen parameters: 255726

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Command line parameters:

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-UNITS=bites -START=1 -END=1 -MATRIX=blomsu62 -TRANS=human40 codi -LIST=150
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-Fgapext=7 -Ygapop=10 -Ygapext=0.5 -Delop=6 -Delext=7

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description

1	5435	65.7	1040	1	CARF_HUMAN	Q2h29 homo sapien	58	268	3.2	1453	1	CA11_CHICK	P02457 gallus galli
2	4183	50.6	1020	1	CARF_MOUSE	Q2k30 mus musculu	59	268	3.2	1459	1	CA12_MOUSE	P28481 mus musculu
3	1209.5	14.6	953	1	CAR4_MOUSE	Q2h80 mus musculu	60	267	3.3	1355	1	CA21_RANCA	O42350 rana catesb
4	1196.5	14.5	953	1	CAR4_HUMAN	Q2y239 homo sapien	61	264	3.2	1669	1	CA14_HUMAN	P02462 homo sapien
5	523	6.3	1062	1	PVA7_HUMAN	P59046 homo sapien	62	263	3.2	1496	1	CA25_HUMAN	P03597 homo sapien
6	495.5	6.0	1033	1	C1S1_MOUSE	Q2r48 mus musculu	63	263	3.2	1669	1	CA14_MOUSE	P02463 mus musculu
7	494.5	6.0	1034	1	C1S1_HUMAN	Q2r48 mus musculu	64	262	3.2	1665	1	CA54_HUMAN	P29400 homo sapien
8	429	5.2	1130	1	C2T4_HUMAN	P33076 homo sapien	65	261.5	3.2	1685	1	CA12_HUMAN	P02458 homo sapien
9	417.5	5.0	1155	1	C2T4_MOUSE	P79602 mus musculu	66	259.5	3.1	1362	1	CA21_CHICK	P02453 gallus galli
10	407	4.9	1473	1	NAL4_HUMAN	Q2m22 mus musculu	67	259	3.1	779	1	CA11_BOVIN	P02457 gallus galli
11	382	4.7	994	1	PVA5_HUMAN	Q2m22 mus musculu	68	258.5	3.1	1763	1	CA24_ASCU	P27393 ascaris suu
12	385.5	4.7	854	1	PVA5_RAT	Q2m22 mus musculu	69	258	3.1	456	1	RINI_PIG	P10773 sus scrofa
13	382	4.6	1062	1	NAL2_HUMAN	Q2m22 mus musculu	70	258	3.1	1366	1	CA21_HUMAN	P08123 homo sapien
14	374.5	4.5	980	1	PVA3_HUMAN	P59044 homo sapien	71	257	3.1	1372	1	CA21_MOUSE	Q01149 mus musculu
15	366	4.4	892	1	PVA5_HUMAN	Q2r48 mus musculu	72	256.5	3.1	1806	1	CA1B_HUMAN	P12107 homo sapien
16	360.5	4.4	843	1	PVA5_MOUSE	Q2r48 mus musculu	73	255.5	3.1	1838	1	CA15_HUMAN	P20908 homo sapien
17	357	4.3	1111	1	MARE_MOUSE	P59047 mus musculu	74	255.5	3.1	1364	1	CA21_BOVIN	P02465 bos taurus
18	342.5	4.1	1200	1	MARE_HUMAN	P59047 mus musculu	75	254	3.1	1366	1	CA28_HUMAN	O46392 bos taurus
19	338	4.1	1466	1	CA13_HUMAN	P02461 homo sapien	76	254	3.1	1736	1	CA28_HUMAN	O46392 bos taurus
20	329.5	4.0	1453	1	CA11_MOUSE	P11087 mus musculu	77	252	3.0	1660	1	YH11_BEV	P13942 homo sapien
21	322.5	3.9	2944	1	CA17_HUMAN	Q02388 homo sapien	78	252	3.0	1366	1	CA1B_MOUSE	P03181 epstein-bar
22	318	3.9	1464	1	CA13_MOUSE	P05397 homo sapien	79	251.5	3.0	1804	1	CA1F_HUMAN	O61245 mus musculu
23	315.5	3.8	1496	1	CA25_HUMAN	P02452 homo sapien	80	250	3.0	1670	1	CA12_BOVIN	Q01955 bos taurus
24	312.5	3.8	1464	1	CA25_HUMAN	P14728 xanthomonas	81	249.5	3.0	1798	1	CA24_CAEEL	P02459 bos taurus
25	312	3.8	784	1	YAN2_HUMAN	P02461 mus musculu	82	249.5	3.0	1804	1	CA24_CAEEL	O61245 mus musculu
26	310.5	3.8	1466	1	YAN2_XANCV	P02461 mus musculu	83	249.5	3.0	1804	1	CA1B_MOUSE	O61245 mus musculu
27	309	3.7	1033	1	CA13_HUMAN	P02461 mus musculu	84	246.5	3.0	1603	1	CA1F_HUMAN	O61245 mus musculu
28	309	3.7	1372	1	PVA6_HUMAN	Q01149 mus musculu	85	244.5	3.0	1362	1	CA21_CHICK	Q07092 homo sapien
29	308.5	3.8	660	1	CA13_MOUSE	P03181 epstein-bar	86	244.5	3.0	1747	1	CA12_BOVIN	P02467 gallus galli
30	307.5	3.7	1464	1	CA13_MOUSE	P08121 mus musculu	87	243	3.0	1285	1	MUC1_HUMAN	P04453 bos taurus
31	305	3.7	1049	1	CA13_BOVIN	P04258 bos taurus	88	243	3.0	1516	1	CA21_ONCVY	P15941 h. mucin 1 p
32	304.5	3.7	1460	1	CA13_BOVIN	P04258 bos taurus	89	242.5	2.9	1712	1	CA24_HUMAN	O93484 oncorhynch
33	301.5	3.7	1418	1	CA11_CANFA	Q2x517 canis famli	90	241.5	2.9	1763	1	CA24_HUMAN	P03572 homo sapien
34	297.5	3.6	1685	1	CA54_HUMAN	P02458 homo sapien	91	241.5	2.9	1763	1	CA24_HUMAN	P03572 homo sapien
35	294.5	3.6	1049	1	CA13_BOVIN	P29400 homo sapien	92	241.5	2.9	1763	1	CA24_HUMAN	P03572 homo sapien
36	294	3.6	779	1	CA11_BOVIN	P02458 bos taurus	93	240.5	2.9	1744	1	CA18_ASCU	P08572 ascaris suu
37	292.5	3.5	1670	1	CA34_HUMAN	O01955 bos taurus	94	239	2.9	1365	1	CA21_RANCA	P14282 oryctolagus
38	290.5	3.5	1262	1	CA13_CHICK	F12105 gallus galli	95	239	2.9	2003	1	NTC4_HUMAN	O42350 rana catesb
39	288	3.5	1366	1	CA21_HUMAN	P08123 homo sapien	96	238.5	2.9	1707	1	CA24_MOUSE	P08122 mus musculu
40	288	3.5	1262	1	CA13_CHICK	F12105 gallus galli	97	238	2.9	1758	1	SPD2_NEPCL	O99466 homo sapien
41	288	3.5	1736	1	CA28_HUMAN	P13942 homo sapien	98	237	2.9	1736	1	CA24_CAEEL	P46804 nephila cia
42	287	3.5	1690	1	CA44_HUMAN	P53420 homo sapien	99	236.5	2.9	1224	1	CA19_HUMAN	Q64733 mus musculu
43	286.5	3.5	1690	1	CA44_HUMAN	P53420 homo sapien	100	236.5	2.9	1224	1	CA19_HUMAN	Q64733 mus musculu
44	283.5	3.4	2944	1	CA17_HUMAN	P02458 homo sapien	101	235.5	2.8	1356	1	CA21_ONCVY	Q93484 oncorhynch
45	281.5	3.4	1364	1	CA21_BOVIN	P02463 bos taurus	102	235	2.8	1707	1	CA24_MOUSE	P08122 mus musculu
46	281	3.4	671	1	CA11_RAT	P02453 rattus norv	103	233.5	2.8	815	1	PY60_DROME	O93948 dirosophila
47	280	3.4	1459	1	CA12_MOUSE	P02453 rattus norv	104	233.5	2.8	1003	1	MEB6_HUMAN	Q93948 dirosophila
48	278.5	3.4	1372	1	CA21_RAT	P02466 rattus norv	105	233.5	2.8	1691	1	CA14_MOUSE	P02463 mus musculu
49	277.5	3.4	1460	1	CA11_CANFA	Q2x517 canis famli	106	232	2.8	1591	1	CA54_HUMAN	Q14031 homo sapien
50	277.5	3.4	1453	1	CA1B_HUMAN	P12107 homo sapien	107	231	2.8	754	1	5E5_RAT	Q28247 canis famli
51	277	3.3	1453	1	CA15_CHICK	P02457 gallus galli	108	228	2.8	1465	1	CA54_CANFA	O63003 pseudorbie
52	274	3.3	1453	1	CA15_HUMAN	P20308 homo sapien	109	228	2.8	1465	1	CA54_CANFA	O63003 pseudorbie
53	273.5	3.3	1453	1	CA11_MOUSE	P11087 mus musculu	110	227.5	2.8	460	1	RINI_PRYKA	P33749 homo sapien
54	270	3.3	1464	1	CA11_HUMAN	P02455 mus musculu	111	225.5	2.7	1027	1	CARF_RIPPA	P33749 homo sapien
55	268.5	3.2	1372	1	CA21_RAT	P02466 rattus norv	112	225.5	2.7	2142	1	BAT2_HUMAN	P46634 filitla pach
56	268.5	3.3	1603	1	CA1F_HUMAN	Q07092 homo sapien	113	225	2.7	911	1	CA1B_BOVIN	Q28083 bos taurus
57	268.5	3.3	1736	1	CA2B_MOUSE	Q64733 mus musculu	114	223	2.7	1669	1	CA14_HUMAN	P02462 homo sapien

115	224	2.7	1403	1	B1F_MOUSE	Q931b6 mus musculus
116	223	2.7	1527	1	CAH_MOUSE	P39061 mus musculus
117	222.5	2.7	1466	1	IE18_PRIVA	P33479 pseudorabie
118	222	2.7	671	1	CA11_RAT	P02454 rattus norv
119	221.5	2.7	2321	1	NCT3_HUMAN	Qum47 homo sapien
120	220.5	2.7	1461	1	IE18_PRIVT	P1675 pseudorabie
121	219.5	2.7	743	1	CA18_MOUSE	Q00760 mus musculus
122	219.5	2.7	744	1	CA18_HUMAN	P27658 homo sapien
123	219.5	2.7	1712	1	CA24_HUMAN	P08572 homo sapien
124	219	2.6	456	1	RIN1_RAT	P29315 rattus norv
125	218.5	2.6	911	1	CA1B_BOVIN	Q28083 bos taurus
126	218.5	2.6	2161	1	SHK1_HUMAN	Q95666 homo sapien
127	217.5	2.7	1516	1	CA1H_HUMAN	P39060 homo sapien
128	217.5	2.7	2161	1	SHK1_HUMAN	Q95666 homo sapien
129	216.5	2.6	867	1	SRPO_BOVIN	P88167 bos taurus
130	215.5	2.6	1402	1	B1RG_MOUSE	Q931b3 mus musculus
131	215	2.6	635	1	CA28_HUMAN	P25067 homo sapien
132	215	2.6	689	1	CA29_HUMAN	Q14055 homo sapien
133	214.5	2.6	635	1	CA29_HUMAN	P25067 homo sapien
134	214.5	2.6	1185	1	DRP1_HUMAN	P54259 homo sapien
135	214.5	2.6	1324	1	IRS2_HUMAN	Q94422 homo sapien
136	214	2.6	1756	1	CA14_CAEEL	P17139 caenorhabdi
137	213.5	2.6	1027	1	CAFT_RIFPA	P30734 riftia pach
138	212.5	2.6	825	1	CA19_HUMAN	P20949 homo sapien
139	212	2.6	825	1	ICP0_HSV2H	P28584 herpes simp
140	212	2.6	1691	1	CA64_HUMAN	Q14031 homo sapien
141	210	2.6	684	1	CA39_HUMAN	Q14050 homo sapien
142	209.5	2.5	684	1	CA39_HUMAN	Q14050 homo sapien
143	209.5	2.6	1336	1	W146_HUMAN	Q90038 homo sapien
144	209.5	2.5	1403	1	B1R4_MOUSE	Q90038 homo sapien
145	209.5	2.6	1756	1	CA14_CAEEL	P17139 caenorhabdi
146	209	2.5	5703	1	M03B_HUMAN	Q94084 homo sapien
147	208.5	2.5	921	1	CA19_MOUSE	Q05722 mus musculi
148	208.5	2.5	2167	1	SHK1_RAT	Q94448 rattus norv
149	208	2.5	680	1	CA1A_HUMAN	Q03692 homo sapien
150	207.5	2.5	1964	1	N1C4_MOUSE	P31695 mus musculi

ALIGNMENTS

RESULT 1	
CAFE_HUMAN	
ID CAFE_HUMAN	STANDARD; PRT; 1040 AA.
AC Q9HC29; Q9GRH5; Q9GRH6; Q9GRH8;	
DT 28-FEB-2003 (rel. 41, Created)	
DT 28-FEB-2003 (rel. 41, Last sequence update)	
DT 15-SEP-2003 (rel. 42, Last annotation update)	
DE Caspase recruitment domain protein 15 (Nod2 protein) (Inflammatory bowel disease protein 1).	
DE CARD15 OR NOD2 OR IBD1.	
GN Homo sapiens (Human).	
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX NCBTaxID=9606;	
RN (1)	
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), MUTAGENESIS OF LYS-305, AND VARIANT ARG-308.	

RC	TISSUE=Breast;
RP	PubMed=11087742;
RA	Ogura Y., Inohara N., Benito A., Chen F.F., Yamaoka S., Nunez G.;
RT	"Nod2, a Nod1/Apaf-1 family member that is restricted to monocytes and activates NF-kappaB."
RL	J Biol. Chem. 276:4812-4818(2001).
RI	[2]
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), VARIANTS CD THR-140; ARG-157;
RP	CYS-235; ARG-248; SER-268; SER-289; ASN-291; VAL-301; TRP-311;
RP	VAL-348; ARG-352; CYS-373; SER-414; LEU-431; VAL-432; LYS-441;
RP	VAL-612; THR-612; TRP-654; TRP-702; CYS-703; CYS-713; GLY-725;
RP	VAL-755; VAL-758; LYS-778; MET-793; LYS-843; SER-853; VAL-863;
RP	ARG-908; ASP-918; ASP-924; AND ILE-955, VARIANTS ULCERATIVE COLITIS
RP	THR-140 AND THR-685, AND VARIANT MET-189.
RC	TISSUE=Leukocyte;
RA	MEDLINE=21279172; PubMed=11385576;
RA	Hugot J.-P., Chamaillard M., Zouali H., Lesage S., Cezard J.-P.,
RA	Belache J., Almer S., Tysk C., O'Morain C.A., Gassull M., Binder V.,
RA	Finkel Y., Cortot A., Modigliani R., Laurent-Puig P.,
RA	Gower-Rousseau C., Macry J., Colombel J.-F., Sabalet M., Thomas G.;
RT	"Association of NOD2 leucine-rich repeat variants with susceptibility to Crohn's disease."
RI	Nature 411:599-603(2001).
RL	[3]
RP	VARIANTS BS GLN-334; TRP-334 AND PHE-469.
RP	MEDLINE=21419644; PubMed=11528384.
RA	McCelli-Richard C., Lesage S., Rybojad M., Prieur A.M.,
RA	Manouvrier-Hanu S., Harner R., Chamaillard M., Zouali H., Thomas G.,
RA	Hugot J.-P.;
RT	"CARD15 mutations in Blau syndrome."
RL	Nat. Genet. 29:19-20(2001).
CC	-1- FUNCTION: Induces NF-kappaB via RICK (CARDIAX, RIP2) and IKK-gamma. Confers responsiveness to intracellular bacterial lipopolysaccharides (LPS).
CC	-1- SUBUNIT: Binds to RICK by CARD-CARD interaction.
CC	-1- SUBCELLULAR LOCATION: Cytoplasmic.
CC	-1- ALTERNATIVE PRODUCTS:
CC	Event=Alternative Initiation;
CC	Comment=2 isoforms, 1/Nod2 (shown here) and 2/Nod2b, are produced by alternative initiation. Both isoforms can activate NF-kappaB. Isoform 1 is more abundant;
CC	-1- TISSUE SPECIFICITY: Monocytes-specific.
CC	-1- DISEASE: Defects in CARD15 are the cause of Blau syndrome (BS) [MIM:186580], a rare autosomal dominant disorder characterized by early-onset granulomatous arthritis, uveitis and skin rash.
CC	-1- DISEASE: Defects in CARD15 are a cause of susceptibility to Crohn's disease (CD) [MIM:266600], a form of remitting inflammatory bowel disease. CD may involve all part of the gastrointestinal tract, but most frequently the terminal ileum and colon. Bowel inflammation is transmural and discontinuous. Crohn's disease is commonly classified as autoimmune disease.
CC	-1- DISEASE: Defects in CARD15 are a cause of susceptibility to ulcerative colitis [MIM:191390], a chronic inflammatory bowel disease. In ulcerative colitis, the inflammation is continuous and limited to rectal and colonic mucosal layers. Ulcerative colitis is commonly classified as autoimmune disease.
CC	-1- SIMILARITY: Contains 2 CARD domains.

CC -1- SIMILARITY: Contains 1 NACHT domain.
CC -1- SIMILARITY: Contains 6 leucine-rich (LRR) repeats.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL: AF178930; AAG3677.1; -.
DR EMBL: AF385089; AAK70867.1; -.
DR EMBL: AF385090; AAK70868.1; -.
DR EMBL: AJ303140; CAC42117.1; -.
DR Genew: HGNC:5331; CARD15.
DR MIM: 605956; -.
DR MIM: 186580; -.
DR MIM: 266600; -.
DR MIM: 191390; -.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR007091; LRR_RNinh.
DR InterPro: IPR007111; NACHT_NTPase.
DR Pfam: PF00560; LRR; 2.
DR SMART: SM00114; CARD; 1.
DR PROSITE: PS50209; CARD; 2.
DR PROSITE: PS50837; NACHT; 1.
KW ATP-binding; Repeat; Leucine-rich repeat; Disease mutation;
KW Alternative initiation; Polymorphism.
FT CHAIN 1 1040 CASPASE RECRUITMENT DOMAIN PROTEIN 15,
FT FT ISOFORM 1.
FT FT CASPASE RECRUITMENT DOMAIN PROTEIN 15,
FT FT ISOFORM 2.
FT FT FOR ISOFORM 2.
FT INIT MET 28 28
FT DOMAIN 26 122 CARD 1.
FT DOMAIN 126 218 CARD 2.
FT DOMAIN 293 618 NACHT.
FT NP BIND 299 306 ATP (POTENTIAL).
FT REPEAT 786 812 LRR 1.
FT REPEAT 814 837 LRR 2.
FT REPEAT 842 865 LRR 3.
FT REPEAT 926 949 LRR 4.
FT REPEAT 954 977 LRR 5.
FT REPEAT 982 1005 LRR 6.
FT VARIANT 140 140 A -> T (in CD and ulcerative colitis).
FT FT /FTid=VAR_012665.
FT VARIANT 157 157 W -> R (in CD).
FT FT /FTid=VAR_012666.
FT VARIANT 189 189 T -> M.
FT FT /FTid=VAR_012667.
FT VARIANT 235 235 R -> C (in CD).
FT FT /FTid=VAR_012668.
FT VARIANT 248 248 L -> R (in CD).
FT FT /FTid=VAR_012669.
FT VARIANT 268 268 P -> S.
FT FT /FTid=VAR_012670.
FT FT
FT VARIANT 289 289 N -> S.
FT FT /FTid=VAR_012671.
FT VARIANT 291 291 D -> N (in CD).
FT FT /FTid=VAR_012672.
FT VARIANT 294 294 T -> S (in CD).
FT FT /FTid=VAR_012673.
FT VARIANT 301 301 A -> V (in CD).
FT FT /FTid=VAR_012674.
FT VARIANT 311 311 R -> W (in CD and
FT FT /FTid=VAR_012675.
FT VARIANT 334 334 R -> Q (in BS).
FT FT /FTid=VAR_012676.
FT VARIANT 334 334 R -> W (in BS).
FT FT /FTid=VAR_012677.
FT VARIANT 348 348 L -> V (in CD).
FT FT /FTid=VAR_012678.
FT VARIANT 352 352 H -> R (in CD).
FT FT /FTid=VAR_012679.
FT VARIANT 373 373 R -> C (in CD).
FT FT /FTid=VAR_012680.
FT VARIANT 414 414 N -> S (in CD).
FT FT /FTid=VAR_012681.
FT VARIANT 431 431 S -> L (in CD).
FT FT /FTid=VAR_012682.
FT VARIANT 432 432 A -> V (in CD).
FT FT /FTid=VAR_012683.
FT VARIANT 441 441 E -> K (in CD).
FT FT /FTid=VAR_012684.
FT VARIANT 469 469 L -> F (in BS).
FT FT /FTid=VAR_012685.
FT VARIANT 612 612 A -> T (in CD).
FT FT /FTid=VAR_012686.
FT VARIANT 612 612 A -> V (in CD).
FT FT /FTid=VAR_012687.
FT VARIANT 684 684 R -> W (in CD).
FT FT /FTid=VAR_012688.
FT VARIANT 702 702 R -> W (risk factor for CD).
FT FT /FTid=VAR_012689.
FT VARIANT 703 703 R -> C (in CD and ulcerative colitis).
FT FT /FTid=VAR_012690.
FT VARIANT 713 713 R -> C (in CD).
FT FT /FTid=VAR_012691.
FT VARIANT 725 725 A -> G (in CD).
FT FT /FTid=VAR_012692.
FT VARIANT 755 755 A -> V (in CD and ulcerative colitis).
FT FT /FTid=VAR_012693.
FT VARIANT 758 758 A -> V (in CD).
FT FT /FTid=VAR_012694.
FT VARIANT 778 778 E -> K (in CD).
FT FT /FTid=VAR_012695.
FT VARIANT 793 793 V -> M (in CD).
FT FT /FTid=VAR_012696.
FT VARIANT 843 843 E -> K (in CD).
FT FT /FTid=VAR_012697.
FT VARIANT 853 853 N -> S (in CD).
FT FT /FTid=VAR_012698.
FT VARIANT 863 863 M -> V (in CD).

FT VARIANT 885 885 /FtId=VAR_012699.
A -> T (in ulcerative colitis).
Ft /FtId=VAR_012700.
FT VARIANT 908 908 G -> R (in CD).
Ft /FtId=VAR_012701.
FT VARIANT 918 918 A -> D (risk factor for CD).
Ft /FtId=VAR_012702.
FT VARIANT 924 924 G -> D (in CD).
Ft /FtId=VAR_012703.
FT VARIANT 955 955 V -> I.
Ft /FtId=VAR_012704.
FT MUTAGEN 305 K -> R: NO ACTIVATION.
SQ SEQUENCE 1040 AA; 115282 MW; 0037592D96D7DDEF CRC64;

Alignment Scores:
Pred. No.: 3,91e-295 Length: 1040
Score: 5435.00 Matches: 1040
Percent Similarity: 99.90% Conservative: 0
Best Local Similarity: 99.90% Mismatches: 0
Query Match: 65.72% Indels: 1
DB: 1 Gaps: 0

US-10-014-269-33 (1-4486) x CARF_HUMAN (1-1040)

QY 106 ATGGGGAAGAGGGGTGTCAGCCTCTCACATGAGAGAAAGAGCAATGTCCTCTC 165
Db 1 MetGlyGluGluGlyGlySerHisAspGluGluArgHisSerValLeuLeu 20

QY 166 GACATCTCCGGGTTGTGAATGCTGCGAGAGGCTTTTCAGGACAGAGAGCCAG 225
Db 21 GlyHisSerProGlyCysGluMetCysSerGlnGluAlaPheGlnAlaGluArgSerGln 40

QY 226 CTGGTCAGAGCTGCTGGTCTCAGGGTCCTCGAGAGGCTTCAGAGTGTCTGGAGTGGCTG 285
Db 41 LeuValGluLeuLeuValSerGlySerLeuGluGlyPheGluSerValLeuAspTyrPheLeu 60

QY 286 CTGTCTGGAGAGGTCCTCTCTCTGGAGAGACTACAGAGGCTTCACCTCCTGGAGCCAGCT 345
Db 61 LeuSerTyrGluValLeuSerTyrGluAspTyrGluGlyPheHisLeuLeuGlyGlnPro 80

QY 346 CTCTCCCACTTGGCGAGGGGCTCTGGACACCGCTCGAATTAAGGGTACTGGGCTGT 405
Db 81 LeuSerHisLeuValAlaArgTyrLeuLeuAspTyrValTyrPheGlnGlyTyrTyrPheAlaCys 100

QY 406 CAGAAAGTCATCGCGGCTGCCCAAGAGGCCAGAGCCAGACCTGCCGCCCAAGTCGAT 465
Db 101 GlnLysLeuIleAlaAlaGlnGluAlaGlnAlaAspSerGlnSerProLysLeuHis 120

QY 466 GGCTGCTGGAGCCCGCACTCGCTCCACCCAGCCCGAGACCTGCGAGTCAACCGGAGCC 525
Db 121 GlyCysTyrPheAspProHisSerLeuHisSerProAlaArgAspLeuGlnSerHisArgProAla 140

QY 526 ATTGTCAAGAGGCTCCACAGGCAATGTGAGGAACATCTGAGACTGGCATGGAGGCGGGCT 585
Db 141 IleValAlaArgTyrLeuHisSerHisValGluLysMetLeuAspLeuAlaTyrGluAlaGly 160

QY 586 TTCTCAGCCAGATATGAAATGATGAATTCAGGTTCCCAATCTTCACACCGTCCCAAGG 645

Db 161 PheValSerGlnTyrGluCysAspGluIleArgLeuProIlePheThrProSerGlnArg 180

QY 646 GCAAGAGGCTGCTTATCTGCCACGCTGAAGACCAATGATGGCTGCTCTCTTA 705
Db 181 AlaArgTyrLeuLeuAspLeuAlaThrValLysAlaAsnGlyLeuAlaIlePheLeu 200

QY 706 CAACATGTCAGAGATTAACAGTCCCATGGCCCTGCTTGAAGCTGCCACATGCAAG 765
Db 201 GlnHisValGlnGluLeuProValPheLeuAlaLeuProLeuGluAlaAlaThrCysLys 220

QY 766 AAGTATAGCCCAAGTGAAGACCAACGCTGTCTGCTCAAGTCTGCTCACTAGCTAT 825
Db 221 LysTyrMetAlaLysLeuArgThrThrValSerAlaGlnSerArgPheLeuSerThrTyr 240

QY 826 GATGAGCAGAGACGCTGCTGAGAGACATATACAGAGAAATGCTCGAGAGCTGG 885
Db 241 AspGlyAlaGluThrLeuCysLeuGluAspIleTyrThrGluAsnValLeuGluValTyr 260

QY 886 GCAGATGTGGGCACTGGCTGACCCCGCAGAGAGCCACCTGGGCTTGAAGAG 945
Db 261 AlaAspValGlyMetAlaGlyProProGlnLysSerProAlaThrLeuGlyLeuGlu 280

QY 946 CTCTTCAGACCCCTGGCCACTCAATGACATCGGACACTGTGCTGGTGGGTACG 1005
Db 281 LeuPheSerThrProGlyHisLeuAsnAspAspAlaAspThrValLeuValAlaGlyGlu 300

QY 1006 GCGGCAATGTCAGAGACGCTCCTGACAGGCGCTGCACTGTGTGGGCTGCGAGGCA 1065
Db 301 AlaGlySerGlyLysSerThrLeuLeuGlnArgLeuHisLeuLeuThrPheAlaGlyGln 320

QY 1066 GACTTCAGAGAAATTTCTTTTGTCTTCCACTTACGCTCCGAGCACTGCATGGCTG 1125
Db 321 AspPheGlnGluThrLeuPheValAlaPheProPheSerCysArgGlnLeuGlnCysMetAla 340

QY 1126 AAACCACTCTGTGCGGACTACTCTTGAACACTGTGTGGGCTGAGTGGTCA 1185
Db 341 LysProLeuSerValArgThrLeuLeuPheGluHisCysCysTyrProAspValGlyGln 360

QY 1186 GAAAGCATCTTCCAGTTACTCTTACCAACCTGACCGGTCTGTAACTTTGATGGC 1245
Db 361 GluAspIlePheGlnLeuLeuAspHisProAspArgValLeuLeuThrPheAspGly 380

QY 1246 TTGACAGGTTCAGTTCAGGTTCAAGGATCGTGAACCCACTGCTCCCGACCAACCC 1305
Db 381 PheAspGluPheLysPheValArgThrAspArgGluArgHisCysSerProThrAspPro 400

QY 1306 ACTCTGTCCAGACCTGCTCTTCAACCTTCTGAGGGCAACCTGCTGAAGATGCCGC 1365
Db 401 ThrSerValGlnThrLeuLeuPheAsnLeuLeuGlnGlyAsnLeuLeuLysAsnAlaArg 420

QY 1366 AAGTGGTGAACAGCGCTCCGGCGCTGTGTGGGGTTCTTCAAGAAATGATCGCAC 1425
Db 421 LysValValThrSerArgProAlaIleValSerAlaPheLeuArgLysTyrIleArgThr 440

QY 1426 GAGTCAACCTCAAGGCTTCTGAAACAGGCACTCAAGTGTACTGAGAAAGGCGCAT 1485

Db	441	GLuPheAsnLeuLysGlyPheSerGluGlnGlyIleGluLeuTyrLeuArgLysArgHis	460
QY	1486	CATGAGCCCGGGGGTGGGAGACCGGCTCATCGGCTGCTCCAGAGACCTCAGCCCTGCAC	1345
Db	461	HisGluProGlyValAlaAspArgLeuIleArgLeuGlnGluIleThrSerAlaLeuHis	480
QY	1346	GGTTTGGCCACCTGGCTGTCTCTCATGGATGGTGGCCAAATGCGACCGGAATGTGTG	1605
Db	481	GlyLeuGlyHisLeuProValPheSerThrPheValSerLysGlyHisGlnGluLeu	500
QY	1606	CTGCAGAGGGGGGGTCCCCAAAGACATACAGATATGACTGCTGATTTCTGCAGCAT	1665
Db	501	LeuGlnGluGlyLysSerProLysThrThrAspMetLysLeuIleLeuGlnHis	520
QY	1666	TTTCTGCTGCATGCCACCCCGCCAGACTCAGGTTTCCCAAGCTCTGGAGACCGCTCTCT	1725
Db	521	PheLeuLeuHisAlaThrProProAspSerAlaSerGlnGlyLeuGlyProSerLeuLeu	540
QY	1726	CGGGGCGGCTCCCAACCTCCTGCACCTGGGCAAGCTGGCTGTGGGGGCTGGGCGATG	1785
Db	541	ArgGlyArgLeuProThrLeuLeuHisLeuGlyArgLeuAlaLeuIleProGlyLeuGlyMet	560
QY	1786	TGCTGCTACGTGTCTCAGCCCAAGACTCCAGGCAAGACTCAGCCCTGATGACATT	1845
Db	561	CysCysTyrValPheSerAlaGlnGlnLeuGlnAlaGlnValSerProAspAspIle	580
QY	1846	TCTCTTGGCTTCTGGTGGCTGCCAAAGGTGTGGTGGCGGGAGTACGGGCGCCCTGAAA	1905
Db	581	SerLeuGlyPheLeuValArgAlaLysGlyValValProGlySerThrLapProLeuGlu	600
QY	1906	TTCCCTTCAACATCACTTTCAGTGTCTTCTTGGCGGCTGTACTGGCACTCAGTGTGAT	1965
Db	601	PheLeuHisIleThrPheGlnCysPhePheAlaAlaPheTyrLeuAlaLeuSerAlaAsp	620
QY	1966	GTGCCACCAAGCTTGGTCCAGACCTCTTCAATTGGGCGGCAAGGCAACTCAGCCAAATG	2025
Db	621	ValProProAlaLeuLeuArgHisLeuPheAsnGlyArgProGlyAsnSerProMet	640
QY	2026	GCCAGGCTCCTGGCCACGATGTGCATCCAGGCTCGGAGGGAAGACAGCAGCGGTGGCA	2085
Db	641	AlaArgLeuLeuPheThrPheCysIleGlnAlaSerGlnGlyLysAspSerSerValAla	660
QY	2086	GCTTGGTGCAGAAAGCCGAGCCGACCAACCTTCAATGATCAAGCAAGCTCCTGGCAGGG	2145
Db	661	AlaLeuLeuGlnLysAlaGluProHisAsnLeuGlnIleThrAlaAlaPheLeuAlaGly	680
QY	2146	CTGTGTGCCGGAGAGACTGGGGGCTGCTGGCTGAGTGGCAGACATCTGAGAAAGCCCTG	2205
Db	681	LeuLeuSerArgGluHisIleTrpGlyLeuLeuAlaGluCysGlnHisSerGluLysAlaLeu	700
QY	2206	CTCCGGGCGCAGGGCTGTGCCGCTGGTGTCTGGCCCGACGCTCCGCAAGCACTTCCAC	2265
Db	701	LeuArgArgGlnAlaCysAlaArgTrpCysLeuAlaAspSerLeuArgLysHisPheHis	720
QY	2266	TCCATCCCGCCAGCTGCACCGGGTGAAGCCAGAGGCGTGCATGGCATGGCGGGGTTGATC	2325
Db	721	SerIleProProAlaAlaProGlyGlnAlaLysSerValHisAlaMetProGlyPheIle	740
QY	2326	TGGCTCATCCGAGCCCTGTACAGAGTGCAGAGGAGGAGGCTGGCTCGAAAGGCTGCAGCT	2385
Db	741	TrpLeuIleArgSerLeuTyrGluMetGlnGluLysAlaGlyLeuAlaArgLysAlaAlaArg	760
QY	2386	GGCTTGAATGTTGGGACCTCAAGTTGACATTTTGCAGTGTGGGCCCATGAGTGTGCT	2445
Db	761	GlyLeuAsnValGlyHisLeuLysLeuThrPheCysSerValGlyProThrGluCysAla	780
QY	2446	GGCTTGGGCTTGTGCTGACAGACCTCCGGGGGCGCGGCGCTGCAGCTGGACTGCAC	2505
Db	781	AlaLeuAlaPheValLeuGlnHisLeuArgArgProValAlaLeuGlnLeuAspTyrAsn	800
QY	2506	TCTGGGGTGAACATTGGGCTGGAAGAGCTGCTGGCTGGCTTGGTGTCTGCAGAGCTGTG	2565
Db	801	SerValGlyAspIleGlyValGlnGlnLeuLeuProCysLeuGlyValCysLysAlaLeu	820
QY	2566	TATTGGCCGATACATATCTCAGACCGAGGATCTGCAGGACTCATTGAATGTGCTTT	2625
Db	821	TyrLeuArgAspAsnAsnIleSerAspArgIleCysLysLeuIleGluCysAlaLeu	840
QY	2626	CAGTGCAGCAATTGCAGAAATTAGCTATTCACAAACAATTGACTGAGCGCTGTGCA	2685
Db	841	HisCysGlnGlnLeuGlnLysLeuAlaLeuPheAsnAsnLysLeuThrAspGlyCysAla	860
QY	2686	CAGTCAATGGCTTAACTCTTGCATGCAGGGAAGACTTCTTGGCAATTGAGGCTGGGAAT	2745
Db	861	HisSerValAlaLysLeuLeuAlaCysArgGlnAsnPheLeuAlaLeuArgLeuGlyAsn	880
QY	2746	AACTACATCACTGCGCGGAGGCCCAAGTGTGGCGGAGGGGCTCCGAGGCAACACTCC	2805
Db	881	AsnTyrIleThrAlaAlaGlyAlaGlnValLeuAlaGlnGlyLeuArgLysAsnThrSer	900
QY	2806	TTCAGATTCCCTGGGATTCCTGGGCAACAAGTGGGTGACAGAGGGGCGCAAGCCCTGGCT	2865
Db	901	LeuGlnPheLeuGlyPheIleTrpGlyAsnArgValGlyAspGlnGlyAlaGlnAlaLeuAla	920
QY	2866	GAAAGCTTGGGTGATCAGCAGAGCTTGAAGGTGCTCAGCTGGTGGGGAACAACATTGGC	2925
Db	921	GluAlaLeuGluLysPheLysGlnSerLeuArgTrpLeuSerLeuValGlyAsnAsnIleGly	940
QY	2926	AGTGTGGTCCCAAGGCTTGGCACTGATGCTGGCAAGAACCTCATCTAGAAAGACTC	2985
Db	941	SerValGlyAlaGlnAlaLeuAlaLeuMetLeuAlaLysAsnValMetLeuGluGluLeu	960
QY	2986	TGCTGGAGGAGAAACATCTCCAGGATGAAAGGTGTATGTCTCTCCAGAAAGACTGAG	3045
Db	961	CysLeuGluLysAsnHisLeuGlnAspGlnGlyValCysSerLeuAlaGlnGlyLeuLys	980
QY	3046	AAAAATCAAGTTGAAAAATCCTGAAGTGTCCAAATAACTGCATCAGCTACCTAGAGGGCA	3105
Db	981	LysAsnSerSerLeuLysIleLeuLysLeuSerAsnAsnGlyIleThrTyrLeuGlyAla	1000
QY	3106	GAAAGCTCCTGCAGGCGCCCTTGAAGAAATACACCATCTGGAAGTGTGGCTCCAGAG	3165
Db	1001	GluAlaLeuLeuGlnAla-LeuGluArgAsnAspThrIleLeuGlnValTrpLeuArgGln	1020

QY 3166 GACACTTCTCTAGAGAGGTTTCAAGAGCTGCGTCAAGGACACCAACTCTGCT 3225
DB 1020 yAaHrPhseerIeueSlugIvalAaplySueuIdyQySaAgapThArgLeuLeu 1040
QY 3226 T 3226
DB 1040 u 1040
RESULT 2
CARD_MOUSE STANDARD; PRT: 1020 AA.
AC Q8K320;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Caspase recruitment domain protein 15 (Nod2 protein).
GN CARD15 OR NOD2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=BALB/C; TISSUE=Monocytes;
RA Iwaga Y., Davey M.P., Martin T.M., Planck S.R., Depriest M.L.,
RA Bugn M.M., Suing C., Rosenbaum J.T.;
RT "Cloning, sequencing and expression analysis of the murine Nod2/Card15
RT gene-";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2), AND VARIANTS ALA-212, ARG-240;
RP CYS-422; VAL-485; ALA-603; ILE-675 AND GLN-925.
RC STRAIN=NR1; TISSUE=Breast cancer;
RA MEDLINE=22388297; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Cassavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uscid T.B., Toshiyuki S., Carninci P., Pange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulys S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman A., Madan A., Rodriques S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: Induces NF-kappaB via RICK (CARD14X, RIP2) and IKK-
CC gamma. Confers responsiveness to intracellular bacterial
CC lipopolysaccharides (LPS) (By similarity).
CC

CC -1- SUBUNIT: Binds to RICK by CARD-CARD interaction (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC Name=2; IsoId=Q8K320-1; Sequence=Displayed;
CC IsoId=Q8K320-2; Sequence=VSP_007069, VSP_007070;
CC Note=No experimental confirmation available;
CC -1- SIMILARITY: Contains 2 CARD domains.
CC -1- SIMILARITY: Contains 1 NOD2 domain.
CC -1- SIMILARITY: Contains 10 leucine-rich (LRR) repeats.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@sib-sib.ch).
CC
CC EXBL: AF520774; AA076073.1; -
CC EXBL: BC044774; AA044774.1; AL1_INIT.
CC MGD; MGI:2429397; Card15.
CC InterPro: IPR001315; CARD.
CC InterPro: IPR007091; LRR_N1NH.
CC InterPro: IPR007111; NOD2_NTPase.
CC Pfam: PF00560; LRR_2.
CC
CC PROSITE: PS02029; CARD_2.
CC PROSITE: PS00837; NOD2_1.
CC KW ATP-binding; Repeat; leucine-rich repeat; Polymorphism;
CC RV Alternative splicing.
CC FT DOMAIN 6 104 CARD 1.
FT DOMAIN 106 200 CARD 2.
FT REPEAT 273 600 NOD2.
FT REPEAT 685 709 LRR 1.
FT REPEAT 726 749 LRR 2.
FT REPEAT 766 792 LRR 3.
FT REPEAT 822 845 LRR 4.
FT REPEAT 850 873 LRR 5.
FT REPEAT 882 929 LRR 6.
FT REPEAT 906 929 LRR 7.
FT REPEAT 934 962 LRR 8.
FT REPEAT 963 985 LRR 9.
FT REPEAT 1005 1019 LRR 10.
FT VARSPLIC 1 7 Missing (in isoform 2).
FT VARSPLIC 195 195 /FTId=VSP_007069.
FT VARSPLIC 212 212 E -> EGVSLCSRODGEFTLLICFLIL (in isoform
FT VARSPLIC 240 240 2).
FT VARSPLIC 422 422 T -> A (in strain NR1).
FT VARSPLIC 485 485 Q -> R (in strain NR1).
FT VARSPLIC 603 603 L -> C (in strain NR1).
FT VARSPLIC 675 675 G -> V (in strain NR1).
FT VARSPLIC 925 925 V -> I (in strain NR1).
FT VARSPLIC 925 925 E -> Q (in strain NR1).

SQ SEQUENCE 1020 AA; 113561 MW; 25504905 ECF70FB8 CRC64;

Alignment Scores:
Pred. No.: 8,73e-218 Length: 1020
Score: 4183.00 Matches: 804
Percent Similarity: 87.30% Conservative: 83
Best Local Similarity: 79.13% Mismatches: 128
Query Match: 50.58% Indels: 1
DB: 1 Gaps: 0

US-10-014-269-33 (1-4486) x CARF_MOUSE (1-1020)

QY 181 TGTGAATGTGCTCCAGAGAGGCTTTTCAGGACAGAGAGGACGCTGGTGGAGCTGCTG 240
DB 6 CysaspMecySerGlnGlnGlnPheGlnAlaGlnSerGlnLeuValAlaLeuLeu 25
QY 241 GTCTCAGGGTCCCTGGAAGGCTTCAAGAGTCTGAGACTGACTGCTGCTGGAGGCTC 300
DB 26 ILeSerGlySerLeuGlnGlnGlnGlnSerIleLeuAspTrpLeuLeuSerTrpAspVal 45
QY 301 CTCTCCTGGAGAGACTACAGAGGCTTCCACCTCCTGGGCGAGGCTCTCCACCTTGGCC 360
DB 46 LeuSerArgGlnAspTrpGlnGlnGlnGlnLeuSerLeuProGlnProLeuSerHisSerAla 65
QY 361 AGGCGCTTCTTGAACCGCTCTGGAATTAAGGTACTTGGGCTGTCAAGAGCTCATCGG 420
DB 66 ArgArgLeuLeuAspTrpValTrpAsnGlyGlyValTrpGlyCysGlnGlnLeuGln 85
QY 421 GCTGCCCAAGAGGCGGACAGAGGCTGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
DB 86 AlaValGlnGlnAlaGlnAlaSerHisSerHisSerHisSerHisSerHisSerHisSer 105
QY 481 CACTGCTCCACCCAGCCGAGACCTGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 540
DB 106 HisSerLeuHisSerProThrArgAspLeuGlnSerHisSerHisSerHisSerHisSer 125
QY 541 CACAGCCATGTGGAGAGACATGCTGSACTGGGATGGAGGCGGCTTGTCTACAGCTCAT 600
DB 126 TyrAsnHisValGlnAlaMetLeuGlnLeuAlaArgGlnGlnGlnGlnGlnGlnGlnGln 145
QY 601 GAATGTGATGAATCAAGTTGCCGATCTTCAACCGCTGCCAGAGGCAAGAGGCTGCT 660
DB 146 GlnCysGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 165
QY 661 GATCTTGCACGCTGAAAGGCAATGATGGCTGCTTCTTCAACATGTTCAAGAA 720
DB 166 AspLeuAlaAlaValLysAlaAsnGlyLeuAlaAlaPheLeuLeuGlnHisValArgGln 185
QY 721 TTACAGTCCCATTTGGCTGCTTGGAGGCTGCCACATGCAAGAAATATATGGCAAG 780
DB 186 LeuProAlaProLeuProLeuProGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 205
QY 781 CTGAGGACACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
DB 206 LeuArgThrMetValLeuThrGlnSerArgPheLeuSerTrpTrpAspGlySerGlnAsn 225
QY 841 CTCTGCTGAGGAGACATACACAGAGATGTCTGAGAGTCTGGGAGATGTGGGCTG 900

DB 226 LeuCysLeuGlnAspIleTyrThrGlnAsnIleLeuGlnLeuGlnThrGlnValGlnThr 245
QY 901 GCTGAGCCCGGAGAGAGAGGCGGACCGCTGGGCTGAGAGGCTCTTACAGACCGCT 960
DB 246 AlaGlnAlaLeuGlnGlnSerProAlaIleLeuGlnGlnGlnGlnGlnGlnGlnGlnGln 265
QY 961 GGCACCTCAATGACGATGCCAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
DB 266 GlyHisLeuAsnArgAspAlaAspThrIleLeuValAlaGlnGlnGlnGlnGlnGlnGlnGln 285
QY 1021 AGCAGGCTCCGAGGCTGCACTTGTGTGGGCTGCAAGGCAAGCACTTCCAGAAATT 1080
DB 286 SerThrLeuLeuGlnArgLeuHisLeuLeuTrpAlaTrpGlyArgSerPheGlnGlnPhe 305
QY 1081 CTCTTGTCTTCCCATTTGACCTGCGGAGGCTGCAATGATGCGAAACCACTCTGTG 1140
DB 306 LeuPheIlePheProPheSerCysArgGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 325
QY 1141 CGGACTCACTTGTGAGCACTGCTGTTGGCTGATGTTGGTCAAGAAACATCTTCCAG 1200
DB 326 ArgThrLeuLeuPheGlnHisCysCysTrpProAspValAlaGlnAspAspValPheGln 345
QY 1201 TTACTCTGACCACTGACCGTGTCTGTAACTTTGATGGCTTGAAGAGTTCAAG 1260
DB 346 PheLeuLeuAspHisProAspArgValLeuLeuThrPheAspGlyLeuAspGlnPheLys 365
QY 1261 TTCAGGTTCAAGGATCGTGAAGCAGCTGCTCCCGGACCAACCGCTCTGTCCAGAC 1320
DB 366 PheArgPheThrAspArgGlnArgHisCysSerProIleAspProThrSerValGlnThr 385
QY 1321 CTGCTTTCAACCTTGTGAGGCAACCTGCTGAAGATGGCGGCAAGTGTGACACAGC 1380
DB 386 LeuLeuPheHisLeuLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 405
QY 1381 GGTCCGCGCTGTGTGGGCTTCTCAGAGATCAATCCGACAGGATTCACACTCAAG 1440
DB 406 ArgProAspAlaValSerAlaLeuLeuArgLysPheValArgThrGlnLeuGlnLeuLys 425
QY 1441 GGCTGCTGAACAGGCGATCGAGCTGTGAGAGAGGCGCAATGAGCCGAGGCTG 1500
DB 426 GlyPheSerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 445
QY 1501 GCGAGCGCTCATCCGCTGCTCCAGAGACCTGAGCGCTGACGCTTGTGCCACCTG 1560
DB 446 AlaAspArgLeuIleGlnLeuIleGlnAlaThrSerAlaLeuHisGlyLeuCysHisLeu 465
QY 1561 CCTGTCTTCAATGATGCTGTCCAAATGCCACCAAGAACTGTGCTGCAAGAGGAGGAG 1620
DB 466 ProValPheSerTrpMetValSerArgCysHisArgGlnLeuLeuGlnAsnArgGly 485
QY 1621 TCCCAAAAGACATACAGATATGACTGCTGATCTGAGAGATTTTCTGCTGAGATCC 1680
DB 486 PheProThrThrSerThrAspMetCysLeuLeuIleLeuGlnHisPheLeuLeuHisAla 505
QY 1681 ACCCGCCCAACATCAGCTTCCAGAGCTGCGGACCGCACTTCTTGGGAGCGCTCCCC 1740
DB 1740

Db 506 SerProbaSerSerProLeuGlyProGlyLeuLeuGlnSerArgLeuSer 525
 QY 1741 ACCCTCCTGCACTGGGCAAGACTGGCTCTGTGGGGCTGGGCACTGGCTGCTAGCTGTTG 1800
 Db 526 ThrLeuLeuHISLeuGlyHISLeuAlaLeuArgGlyLeuAlaLeuSerCysTyrValPhe 545
 QY 1801 TCAGCCCAAGCACTCCAGGCAAGCAAGCTCAAGCTGAGCACTTCTGCTGGCTGCTG 1860
 Db 546 SerAlaGlnGlnLeuGlnAlaGlnValAlaSerPhePhePhePhePhePhe 565
 QY 1861 GTGGTGGCAAAAGTGTGTCGCAAGGAGTACGGCCGCTGCAATTCCTGCACTGACT 1920
 Db 566 ValArgAlaGlnSerSerValProGlySerTyrAlaProLeuGlnPheLeuHISLeu 585
 QY 1921 TTCAGTGGCTCTTGGCCGCTGCTAGCTGGGCACTGAGTGGCTGAGTGGCAAGCTTTG 1980
 Db 586 PheGlnCysPhePheAlaPheTyrLeuAlaValSerAlaPheThrSerValAlaSer 605
 QY 1981 CTGAGACACTCTTCAATTGTGGCAAGGCAAGCACTCAACAAATGGCCAGGCTGCTGCC 2040
 Db 606 LeuTyrHISLeuPheSerCysGlyArgLeuGlySerLeuLeuGlyArgLeuLeuPro 625
 QY 2041 ACGATGTGCATCCAGGCTCCAGGGAAGAAGCAAGCAAGCTGGAGCTTGTGTCAGAAAG 2100
 Db 626 AsnLeuCysHISLeuGlySerArgValLysLysGlySerGlnAlaAlaLeuLeuGln 645
 QY 2101 GCCGAGCCGCAACAACCTTCAGATCAAGCAAGCTCTGTCGCAAGGCTGTGTCGCGGAG 2160
 Db 646 AlaGlnProHISAsnLeuGlnHISLeuAlaPheLeuAlaGlyLeuLeuSerGlnGln 665
 QY 2161 CACTGGGCGCTGCTGGCTGAGTGGCAAGCACTGAGAAAGGCGCTGCTCCGGCGCAAGGCC 2220
 Db 666 HisArgAspLeuLeuAlaLeuGlySerGlnValSerGlnValLeuLeuHISAlaArgGlnAla 685
 QY 2221 TGTGCCGCTGCTGCTGCTGGCCCGCAAGCTCCGCAAGCACTTCACCTCCGCGCGAGCT 2280
 Db 686 ArgAlaArgSerCysLeuAlaHISLeuLeuArgGlnHISLeuSerLeuProAla 705
 QY 2281 GCACGGGCTGAGGCAAGGCTGCACTGCCATGCCGCGCTCATCTGAGCTGATCCGAGC 2340
 Db 706 ValProGlyGlnThrLysSerMetHISAlaSerProGlyPheHISLeuLeuArgSer 725
 QY 2341 CTGTACAGATGCAAGGAGGAGGCTGGCTGGGCAAGGCTGCAAGCTGAGCTGATGTTGG 2400
 Db 726 LeuTyrGlnLysSerGlnGlnGlnLeuAlaGlnAlaValArgArgLeuAspHISLeu 745
 QY 2401 CAAGCTCAAGTTGACATTTTGGAGTGTGGCCCACTGAGTGTGCTGCTGGCTTGTG 2460
 Db 746 HisLeuLysLeuThrPheCysArgValGlyProAlaGlnCysAlaAlaLeuAlaPheVal 765
 QY 2461 CTGCAAGCACTCCGGGCGCGCTGGCTGGCTGAGCTGCAACTGCTGTGGGTGACAT 2520
 Db 766 LeuGlnHISLeuGlnArgProValAlaLeuGlnLeuAspTyrAsnSerValGlyAspVal 785
 QY 2521 GAGGTGAGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2580
 Db 786 GlyValGlnGlnLeuArgProCysLeuGlyValCysThrAlaLeuTyrLeuArgAspAsn 805

QY 2581 AATATCTAGACCGAGGCACTCTGCAAGCTCATGATGCTCTGCACTGGCAAGCAATG 2640
 Db 806 AsnLeuSerAspArgGlyAlaArgThrLeuValGlnCysAlaLeuLysGlyGlnLeu 825
 QY 2641 CAAAGTTAGCTCATTCACACAAATTGACTGAGCGGTGTGCACTCCATGGCTAAG 2700
 Db 826 GlnLysLeuAlaLeuPheAsnLysLeuThrAspAlaCysAlaCysSerMetLeuLys 845
 QY 2701 CTGCTGCACTGACGAGCAACTCTGGCACTTGGAGCTGGGGAAATAACTACATCACTGCT 2760
 Db 846 LeuLeuAlaHISLysGlnAsnPheLeuSerLeuLysGlyValGlyAsnMetHISLeuAla 865
 QY 2761 GCGGAGCCCAAGTGTGGCCGAGGAGGCTCCGAGGCAACACTCTGCACTGCTGCGA 2820
 Db 866 AlaGlyAlaGlnValLeuAlaGlnGlyLeuLysSerAsnThrSerLeuLysPheLeuGly 885
 QY 2821 TTCTGGGGCAAGAGTGGTGAAGAGGGGCGCCAGGCTGAGTGAAGCTTGGGTGAT 2880
 Db 886 PheTrpGlyAsnSerValGlyAspLysGlyThrGlnAlaLeuAlaGlnValAlaAsp 905
 QY 2881 CACAGAGCTTGAAGTGGCTCAAGCTGGTGGGGAACAATTGGCAGTGTGGTGGCA 2940
 Db 906 HisGlnAsnLeuLysTrpLeuSerLeuValGlyAsnMetHISLysMetGlyAlaGln 925
 QY 2941 GCGTTGGCACTGATGCTGGCAAGAAAGCTCATCTAGAAAGACTGCTGCTGAGAGAAC 3000
 Db 926 AlaLeuAlaLeuMetLeuGlnLysAsnLysSerLeuGlnGlnLysCysLeuGlnGln 945
 QY 3001 CATCTCAAGATGAAGGTGATGTTCTCTGCAAGAGCACTGAAAGAAATTCAGATTG 3060
 Db 946 HisLysCysAspGlyGlyValTyrSerLeuAlaGlnGlyLeuLysArgAsnSerThrLeu 965
 QY 3061 AAAATCTGAAGTGTGCAATACTGCACTCACTACCTAGGCGCAAGAGCCCTCTCGAG 3120
 Db 966 LysPheLeuLysLeuSerAsnAsnGlyHISLeuTyrArgGlyAlaGlnAlaLeuLeuGln 985
 QY 3121 GCCCTTGAAGGAATGACACCACTCTGGAAGCTGGCTCCGAGGGAACACTTCTCT 3180
 Db 986 AlaLeuSerArgAsnSerAlaLeuGlnValTrpLeuArgGlyAsnThrAspSerLeu 1005
 QY 3181 AAGAGAGTTGACAAAGCTCGGCTGCAAGGCAACAAGACTTGTCTT 3226
 Db 1005 GlnGlnLysGlnThrLeuSerSerArgAspAlaArgLeuLeu 1020

Search completed: January 7, 2004, 19:48:56
 Job time : 435.754 secs

OM nucleic - protein search, using frame_plus_nzp model

Run on: January 7, 2004, 19:25:21 ; Search time 170.769 Seconds

(Without alignments)
1357.774 Million cell updates/sec

Title: US-10-014-269-33

Perfect score: 8270

Sequence: 1 gtagacagatccagcgtcac.....ataacgtttgacgaacac 4486

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 630525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 1661050

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 150 summaries

Command line parameters:

-MODEL=frame+_nzp.model -DEV=xlp

Q=/cgr2_1/USPTO_spool_P/US10014269/runat_07012004_175229_24521/app_query_fasta_1

.9358

-DB=SPRMBL_23 -QFMT=fastan -SUFFIX=rspt -MINMATCH=0.1 -LOOPEXT=0

-DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=50 -MODE=LOCAL

-OUTFMT=ptc -NOR=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000

-USER=US10014269 @CGN 1 1 482 @runat_07012004_175229_24521 -NCPU=6 -ICPU=3

-NO MAP -LARGESUBV -NEG SCORES=0 -WALT -DSBLOCK=100 -LONGLAG

-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6

-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_rhiz:*
8: sp_orselelle:*
9: sp_phase:*
10: sp_planti:*

11: sp_fodent:*
12: sp_virus:*
13: sp_vertibrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4183	50.6	1020	11 QBR320	QBR320 mus musculus
2	1209.5	14.6	953	11 QBRH20	QBRH20 mus musculus
3	1196.5	14.5	953	4 QBRWFS	QBRWFS homo sapien
4	1006	12.2	706	11 QBRU16	QBRU16 mus musculus
5	495.5	6.0	1033	11 QBR458	QBR458 mus musculus
6	483	5.8	892	4 QBRNU4	QBRNU4 mus musculus
7	431.5	5.2	1052	7 QBRGDB	QBRGDB ratu mus norv
8	431.5	5.2	1073	7 QBRGDB	QBRGDB ratu mus norv
9	431.5	5.2	1153	7 QBRGDB	QBRGDB ratu mus norv
10	417.5	5.0	1155	7 QBRP21	QBRP21 mus musculus
11	410.5	5.0	778	4 QBRNF48	QBRNF48 mus musculus
12	380	4.6	713	6 QBRJL27	QBRJL27 mus musculus
13	357.5	4.3	733	4 QBRTE2	QBRTE2 mus musculus
14	354.5	4.3	982	11 QBRU40	QBRU40 mus musculus
15	352.5	4.3	499	4 QBRM13	QBRM13 mus musculus
16	352	4.3	5146	6 QBRM14	QBRM14 mus musculus
17	349.5	4.2	5146	6 QBRM14	QBRM14 mus musculus
18	339.5	4.1	1056	4 QBRNF42	QBRNF42 mus musculus
19	332	4.0	846	4 QBRX10	QBRX10 mus musculus
20	322	3.9	932	4 QBRNF4	QBRNF4 mus musculus
21	321.5	3.9	660	4 QBRNF06	QBRNF06 mus musculus
22	321	3.9	692	4 QBRM14	QBRM14 mus musculus
23	320	3.9	1464	11 QBRM14	QBRM14 mus musculus
24	319	3.9	884	7 QBRM13	QBRM13 mus musculus
25	317	3.9	1222	11 QBRM13	QBRM13 mus musculus
26	316.5	3.8	1787	10 QBRM13	QBRM13 mus musculus
27	316	3.9	4123	4 QBRM13	QBRM13 mus musculus
28	313	3.8	1453	11 QBRM13	QBRM13 mus musculus
29	312.5	3.8	1464	4 QBRM13	QBRM13 mus musculus
30	310.5	3.8	1637	6 QBRM13	QBRM13 mus musculus
31	309	3.8	1464	11 QBRM13	QBRM13 mus musculus
32	308	3.8	1464	11 QBRM13	QBRM13 mus musculus
33	307.5	3.7	977	7 QBRM13	QBRM13 mus musculus
34	307.5	3.7	1222	11 QBRM13	QBRM13 mus musculus
35	306.5	3.7	863	11 QBRM13	QBRM13 mus musculus
36	306.5	3.7	1445	13 QBRM13	QBRM13 mus musculus
37	304.5	3.7	1464	11 QBRM14	QBRM14 mus musculus
38	303.5	3.7	1314	11 QBRM14	QBRM14 mus musculus
39	303	3.7	1347	4 QBRM14	QBRM14 mus musculus
40	303	3.7	774	12 QBRM14	QBRM14 mus musculus

41	c	301	3.7	1118	5	Q9VR13	Q9VR13 drosophila	98	269.5	3.3	1418	6	Q28396	Q28396 equus caball	
42	c	300.5	3.6	1464	11	Q9BR12	Q9BR12 mus musculus	99	268.5	3.2	605	10	Q932V8	Q932V8 arabidopsis	
43	c	300.5	3.7	1953	5	Q9B1T7	Q9B1T7 nephila mad	c 100	268.5	3.3	1838	11	Q98207	Q98207 mus musculus	
44	c	300	3.7	1450	13	Q9Y1B4	Q9Y1B4 cynops pyrr	101	268	3.2	998	11	Q8CFM4	Q8CFM4 mus musculus	
45	c	299.5	3.7	1160	4	Q14046	Q14046 homo sapien	102	268	3.2	1442	11	Q62031	Q62031 mus musculus	
46	c	299	3.6	1447	13	Q91B91	Q91B91 xenopus lae	103	268	3.2	1442	11	Q62033	Q62033 mus musculus	
47	c	299	3.6	1487	6	Q77753	Q77753 canis famli	104	268	3.2	1442	11	Q62032	Q62032 mus musculus	
48	c	298.5	3.6	1487	4	Q14047	Q14047 homo sapien	105	267.5	3.2	1459	11	Q62032	Q62032 mus musculus	
49	c	296	3.6	2703	5	Q9VEG7	Q9VEG7 drosophila	106	267.5	3.2	1626	4	Q9NFW1	Q9NFW1 mus musculus	
50	c	294.5	3.6	1418	6	Q28386	Q28386 equus caball	107	267	3.2	1820	13	Q91B91	Q91B91 xenopus lae	
51	c	294.5	3.6	2944	11	Q63870	Q63870 mus musculus	c 108	266.5	3.2	1439	5	Q97406	Q97406 halictis di	
52	c	292.5	3.6	1682	11	Q9C2R9	Q9C2R9 mus musculus	c 109	266	3.2	1439	5	Q97406	Q97406 halictis di	
53	c	292	3.5	397	11	Q8BJF4	Q8BJF4 mus musculus	c 110	266	3.2	1453	11	Q63079	Q63079 rattus norv	
54	c	292	3.5	886	4	Q9NUB7	Q9NUB7 homo sapien	111	266	3.2	1621	4	Q9H4R9	Q9H4R9 homo sapien	
55	c	292	3.6	1420	13	Q90W37	Q90W37 gallus gall	112	265.5	3.2	1487	4	Q14047	Q14047 homo sapien	
56	c	291.5	3.6	890	12	Q8UZE1	Q8UZE1 ceratopithec	c 113	265.5	3.2	1739	11	Q941L2	Q941L2 mus musculus	
57	c	291	3.5	1414	5	Q26634	Q26634 strongyloce	c 114	264.5	3.2	1352	13	Q90VU0	Q90VU0 brachydanti	
58	c	290	3.5	1580	11	Q8BLX7	Q8BLX7 mus musculus	c 115	264.5	3.2	1835	13	Q91AU4	Q91AU4 gallus gall	
59	c	289.5	3.5	1366	4	Q15177	Q15177 homo sapien	c 116	264	3.2	1840	11	Q60467	Q60467 cricetus	
60	c	289.5	3.5	1442	11	Q62033	Q62033 mus musculus	c 117	263.5	3.2	1491	13	Q91718	Q91718 xenopus lae	
61	c	289.5	3.5	2715	5	Q61603	Q61603 drosophila	c 118	263	3.2	1894	5	Q9MW54	Q9MW54 mytilus gal	
62	c	289.5	3.5	2716	5	Q81N94	Q81N94 drosophila	c 119	262.5	3.2	1160	4	Q14046	Q14046 homo sapien	
63	c	289.5	3.5	4998	11	Q8CC65	Q8CC65 mus musculus	120	262	3.2	195	4	Q8N101	Q8N101 homo sapien	
64	c	289	3.5	1637	6	Q9XSV8	Q9XSV8 bos taurus	c 121	262	3.2	1737	11	Q91U04	Q91U04 rattus norv	
65	c	288.5	3.5	1497	11	Q61431	Q61431 mus musculus	c 122	262	3.2	1827	13	Q8U0N5	Q8U0N5 cryzias lat	
66	c	288	3.5	1097	4	Q9H6V0	Q9H6V0 homo sapien	c 123	261.5	3.2	1684	6	Q8HVC1	Q8HVC1 canis famli	
67	c	287.5	3.5	706	12	Q41972	Q41972 murid herpe	124	261	3.2	1419	11	Q63123	Q63123 rattus norv	
68	c	287.5	3.5	4123	4	Q75851	Q75851 homo sapien	c 125	260.5	3.1	1445	13	Q932S1	Q932S1 rana catesb	
69	c	284.5	3.4	4998	11	Q8CC65	Q8CC65 mus musculus	126	260	3.1	1366	4	Q15177	Q15177 homo sapien	
70	c	284	3.5	1163	4	Q8N6U4	Q8N6U4 homo sapien	127	259	3.1	620	16	Q8XZM9	Q8XZM9 ralsionda s	
71	c	284	3.5	1419	11	Q63123	Q63123 rattus norv	c 128	259	3.2	998	11	Q8CFM4	Q8CFM4 mus musculus	
72	c	284	3.5	1459	11	Q62032	Q62032 mus musculus	c 129	259	3.2	1835	13	Q91AU4	Q91AU4 gallus gall	
73	c	282.5	3.4	1442	11	Q62031	Q62031 mus musculus	130	258.5	3.1	1739	11	Q81U12	Q81U12 mus musculus	
74	c	282	3.4	312	11	Q8BV65	Q8BV65 mus musculus	c 131	258	3.1	1449	13	Q8XW17	Q8XW17 brachydanti	
75	c	282	3.4	1458	13	Q910B9	Q910B9 oncohychnu	c 132	258	3.1	1838	11	Q8E207	Q8E207 mus musculus	
76	c	282	3.4	1669	11	Q9QZS0	Q9QZS0 mus musculus	133	257.5	3.1	2703	5	Q9VEG7	Q9VEG7 drosophila	
77	c	282	3.4	1802	5	Q17163	Q17163 drugia mala	134	257.5	3.1	2715	5	Q61603	Q61603 drosophila	
78	c	281.5	3.4	1626	4	Q8NFW1	Q8NFW1 homo sapien	135	257.5	3.1	2716	5	Q81N94	Q81N94 drosophila	
79	c	281.5	3.4	1664	6	Q8HVC1	Q8HVC1 canis famli	136	257	3.1	1258	13	Q8XW11	Q8XW11 brachydanti	
80	c	281	3.4	1414	5	Q26634	Q26634 strongyloce	137	257	3.1	1314	11	Q8CC65	Q8CC65 mus musculus	
81	c	280	3.4	1838	4	Q15094	Q15094 homo sapien	c 138	256.5	3.1	1691	11	Q9ESQ2	Q9ESQ2 mus musculus	
82	c	279	3.4	1420	13	Q90W37	Q90W37 gallus gall	c 139	256.5	3.1	1691	11	Q9ESQ2	Q9ESQ2 mus musculus	
83	c	278	3.4	727	12	Q41973	Q41973 murid herpe	140	256.5	3.1	1838	4	Q15094	Q15094 homo sapien	
84	c	277.5	3.4	1450	13	Q9Y1B4	Q9Y1B4 cynops pyrr	141	255.5	3.1	1688	13	Q90796	Q90796 gallus gall	
85	c	276.5	3.3	1163	4	Q8N6U4	Q8N6U4 homo sapien	c 142	255.5	3.1	1418	13	Q9W7R9	Q9W7R9 cynops pyrr	
86	c	276	3.3	1745	4	Q9N206	Q9N206 homo sapien	143	255.5	3.1	1491	13	Q91718	Q91718 xenopus lae	
87	c	276	3.4	1840	11	Q91U03	Q91U03 rattus norv	144	254	3.1	1447	4	Q96083	Q96083 mus musculus	
88	c	275	3.3	1682	11	Q9QZR9	Q9QZR9 mus musculus	145	254	3.1	1840	11	Q91U03	Q91U03 rattus norv	
89	c	274	3.3	1449	13	Q910C0	Q910C0 oncohychnu	c 146	253	3.1	966	6	Q93UD1	Q93UD1 sus scrofa	
90	c	274	3.3	1449	13	Q910C0	Q910C0 oncohychnu	147	252.5	3.1	1439	5	Q97406	Q97406 halictis di	
91	c	273	3.3	1461	4	Q76045	Q76045 homo sapien	c 148	252.5	3.1	1486	13	Q91717	Q91717 xenopus lae	
92	c	273	3.3	1464	4	Q8N473	Q8N473 homo sapien	149	252	3.0	1840	11	Q60467	Q60467 cricetus	
93	c	272.5	3.3	1689	11	Q9QZS0	Q9QZS0 mus musculus								
94	c	272.5	3.3	1691	11	Q9ESQ2	Q9ESQ2 mus musculus								
95	c	271	3.3	223	4	Q8N102	Q8N102 homo sapien								
96	c	270.5	3.3	1487	6	Q77753	Q77753 canis famli								
97	c	269.5	3.3	608	12	Q9G5K9	Q9G5K9 herpesvirus								

ALIGNMENTS

ALIGNMENTS

[illegible]

QY 1261 TTCAAGTTCAAGGATGTTGACAGGCACTGCTCCCAACGACCCCACTCTGTGTCAGAC 1320
 Db PheArgPheThrAspArgGluArgHisCysSerProIleAspProIleSerValGlnThr 385
 QY 1321 CTGCTCTTCAACCTCTGCAAGGCGCACTGCTGAAAGATGCGCCCAAGGGTGTGACACAG 1380
 Db LeuLeuPheAsnLeuLeuGlnGlyAsnLeuLeuLeuLysAsnHisAlaCysValLeuThrSer 405
 QY 1381 GTCCGCGCGCTGTGTGCGCGCTCTCCAGAAATCAATCCGACCGAATTCAACCTCAAG 1440
 Db ArgProAspAlaValSerAlaLeuLeuArgGlyPheValArgThrGlnLeuGlnLeuLys 425
 QY 1441 GGCTTCTGTGAACAGGGCATGACCTGTACCTGTAGAGAGACCGCATGAGCGCGGAGTG 1500
 Db GlyPheSerGlnGlnGlnGlyLeuGlnLeuLysArgGlnGlnHisAlaArgGlnProGlyVal 445
 QY 1501 GCGAAGCGGCTCATCCGCGCTGCTCCAAAGAGACTCAAGCCCTGCAAGGTTTGTGCACTG 1560
 Db AlaAspArgLeuIleGlnLeuIleGlnIleThrSerAlaLeuHisGlyLeuCysHisLeu 465
 QY 1561 CCTGTCTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
 Db ProValPheSerTrpMetValSerArgCysHisArgGlnLeuLeuLeuLeuLeuLeuLeuLeu 485
 QY 1621 TCCCAAAAGACATCAAGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
 Db PheProThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 495
 QY 1681 ACCCGCCCAAGCTCAGCTTCCCAAGGCTCGGAGGCCCAAGCTTCTTGCGGCGCGCTCCCG 1740
 Db SerProProAspSerSerProLeuGlnLeuGlyProGlyLeuLeuGlnSerAlaArgLeuSer 525
 QY 1741 ACCCTCTGCACTGAGGCAAGCTGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1800
 Db ThrLeuLeuHisLeuGlnGlnHisLeuAlaLeuArgGlyLeuAlaMetSerCysTyrValPhe 545
 QY 1801 TCAGCCCAAGAGCTCCAGGCAAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 1860
 Db SerAlaGlnGlnLeuGlnGlnAlaAlaGlnValAspSerAspAspIleSerLeuGlnGlyPheLeu 565
 QY 1861 GTGCTGTGCAAAAGT 1920
 Db ValArgAlaGlnSerSerValProGlySerTyrAlaProLeuGlnLeuPheLeuHisIleThr 585
 QY 1921 TTCCAGTGTCTTGTGCGCGCTCTAAGCTGCACTGAGCTGATGCTGCAACAGCTTTG 1980
 Db PheGlnCysPhePheAlaAlaPheTyrLeuAlaValSerAlaAspThrSerValAlaSer 605
 QY 1981 CTGAGACACTCTTCATTTGT 2040
 Db LeuLysHisLeuPheSerCysGlyTyrArgGlnGlySerSerLeuLeuGlnValArgLeuLeuPro 625
 QY 2041 ACGATGTGACTCAAGCGCTCGAGGGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2100
 Db AsnLeuCysIleGlnGlySerArgValLysGlySerGlnAlaAlaLeuLeuGlnLys 645

QY 2101 GCGAGCCGCAACAACCTTTCAGATCAAGAGAGCTTCTGTGAGAGGCTGTGTCCCGGAG 2160
 Db AlaGlnProHisAsnLeuGlnIleThrAlaAlaPheLeuAlaGlyLeuLeuSerGlnGln 665
 QY 2161 CACTGAGGCGCTGCTGGCTGAGTGGCAAGATCTGAGAAAGCGCTGCTCCGGCGCAGGCG 2220
 Db HisAlaGlnPheLeuAlaAlaCysGlnValSerGlnValGlnValLeuLeuGlnAlaGlnAla 685
 QY 2221 TGTGCCGCTGT 2280
 Db ArgAlaArgSerCysLeuAlaHisSerLeuArgGlnHisPheHisSerIleProProAla 705
 QY 2281 GACCGGGGTGAGCCCAAGAGAGCTGCATCCATGCCGGGTTCATCTGCTGATCTCCAGAG 2340
 Db ValProGlnGlnLysSerHisAlaMetProGlyPheIleTrpLeuIleArgSer 725
 QY 2341 CTGTACAGATGCAAG 2400
 Db LeuTyrGlnMetGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 745
 QY 2401 CAGCTCAAGTGAATTTTGCAGTGTGGGCCCACTGAGTGTGCTGCTGCTGCTGCTGCTGCTG 2460
 Db HisLeuLysLeuThrPheCysArgValGlyProAlaGlnCysAlaAlaLeuAlaPheVal 765
 QY 2461 CTGAGCACTCCGGCGCGCGCTGGCGCTGCACTGAGCTACAAGCTGTGGGTGAGCAT 2520
 Db LeuGlnHisLeuGlnArgProValAlaLeuGlnLeuLysArgTyrHisSerValGlyAspVal 785
 QY 2521 GCGTGAAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2580
 Db GlyValGlnGlnLeuArgProCysLeuGlyValCysThrAlaLeuTyrLeuArgAspAsn 805
 QY 2581 AATATCTCAAGCCAGAGAGCTGCAAGCTGATGATGATGATGATGATGATGATGATGATGATG 2640
 Db AsnIleSerPheArgGlyAlaArgThrLeuValGlnCysAlaLeuArgCysGlnGlnLeu 825
 QY 2641 CAGAAATTACTCTATTCACAAACAATTGACTGAGCTGAGCACTGCATGAGCTAAG 2700
 Db GlnLysLeuAlaLeuPheAsnAsnLysLeuThrAspAlaCysAlaCysSerValAlaLys 845
 QY 2701 CTGCTGATGAGGCGAAGCTTCTGTGCAATGAGCTGAGGCGAATTAAGTCACTGCTGCC 2760
 Db LeuLeuAlaHisLysGlnHisPheLeuSerLeuArgValGlyAsnHisIleThrAla 865
 QY 2761 GCGAGACCCCAAGT 2820
 Db AlaGlyAlaGlnValLeuAlaGlnGlnLysSerAsnThrSerLeuLysPheLeuGly 885
 QY 2821 TTCTGAGGCGCAAGAGTGGGTGACAGGAGGCGCCAGGCGCTGAGTGAAGCTTGTGAT 2880
 Db PheTrpGlyAsnSerValGlyAspLysGlyThrGlnAlaLeuAlaGlnValAlaAsp 905
 QY 2881 CACGAGGCTTGAAGTGGCTCAGGCTGAGTGGGAAACAATGAGAGTGTGGGTGCCCA 2940
 Db HisGlnHisLeuLysTrpLeuSerLeuValGlnHisAsnIleGlySerMetGlyAlaGln 925
 QY 2941 GCTTGGCACTGATGCTGGCAAG 3000

and is derived by analysis of the total score distribution.

SUMMARIES

OM protein - protein search, using sw model
Run on: January 7, 2004, 20:04:17 ; Search time 38.0703 seconds
(without alignments)
4223.507 Million cell updates/sec
Title: US-10-014-269-3
Perfect score: 5304
Sequence: 1 MCSQAFQACRSQVLLVLS.....NFTSLEVDKLCGRDRLLL 1013
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 1107863 seqs, 15872653 residues
Total number of hits satisfying chosen parameters: 1107863
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT*
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT*
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT*
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT*
5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT*
6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT*
7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT*
8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT*
9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT*
10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT*
11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT*
12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT*
13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT*
14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT*
15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT*
16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT*
17: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1996.DAT*
18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT*
19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT*
20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT*
21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT*
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,

Result No.	Score	Match	Length	DB	ID	Description
1	5304	100.0	1013	23	AAE25417	Human Nod2 protein
2	5304	100.0	1013	23	ABJ04736	Nod2b protein wild
3	5304	100.0	1040	23	AAE25416	Human Nod2 protein
4	5303	100.0	1040	23	ABJ04773	Nod2a V9551 protei
5	5301	99.9	1040	23	ABJ04771	Nod2a V953M protei
6	5300	99.9	1040	23	ABJ04774	Nod2a W633V protei
7	5299	99.9	1040	23	AAE25418	Human Nod2 protein
8	5299	99.9	1040	23	ABJ04737	Nod2 protein sequ
9	5299	99.9	1040	23	ABJ04772	Nod2a N852S protei
10	5296	99.8	1038	23	ABJ04735	Nod2a protein wild
11	5296	99.8	1040	23	ABJ04768	Nod2a R702W protei
12	5296	99.8	1040	23	ABJ04769	Nod2a G908R (SNP17
13	5296	99.8	1040	23	ABJ04770	Nod2a P268S protei
14	5296	99.8	1041	22	AAE25419	Amliro acid sequenc
15	5291	99.8	1040	23	ABJ04776	Nod2a P268S + N852
16	5288	99.7	1040	23	ABJ04775	Nod2a P268S + G980
17	5288	99.7	1040	23	ABJ04777	Nod2a P268S + R702
18	5128	96.7	1007	23	AAE25434	Human Nod2 mutant.
19	5128	96.7	1007	23	ABJ04766	Nod2a protein delt
20	5120	96.5	1007	23	ABJ04767	Nod2a P268S + fram
21	4980.5	93.9	1009	23	AAU80865	Human CARD3X prote
22	4174	78.7	795	23	AAU80875	Human CARD3X prote
23	2945	55.5	560	23	AAU80856	Human CARD3X prote
24	2087	39.3	403	23	AAU80870	Human CARD3X ANG10
25	1614	30.4	305	23	AAE25421	Human Nod2 protein
26	1614	30.4	305	23	ABJ04740	Nod2 nucleotide bi
27	1564	29.5	296	23	AAU80869	Human CARD3X NB-AR
28	1219.5	23.0	953	20	AAV31145	Murine CARD-4L pro
29	1219.5	23.0	953	22	AAE26004	Mouse CARD-4L (lon
30	1219.5	23.0	953	23	ABG31080	Mouse caspase recr
31	1219.5	23.0	953	23	AAO22156	Protein of murine
32	1219.5	23.0	953	24	ABU56298	Mouse Caspase recr
33	1212	22.9	953	22	AAV79473	Human protein SEQ
34	1209.5	22.8	953	21	AAE15552	Apoptosis related
35	1209.5	22.8	953	22	AAV78489	Human protein SFO
36	1209.5	22.8	953	22	AAE20080	Human CARD-4L (lon
37	1208.5	22.8	953	23	AAO22111	Protein of human C
38	1209.5	22.8	953	24	ABU56273	Human Caspase recr
39	1208.5	22.8	953	23	ABG31076	Human Caspase recr
40	1204.5	22.7	953	20	AAV31141	Human CARD-4L prot
41	1171	22.1	966	24	ABU56300	Caspase recruitment
42	1001	18.9	705	21	AAE15559	Apoptosis related
43	1001	18.9	705	21	AAE15562	Fragment of apopto
44	1001	18.9	719	22	AAE75559	Human colon cancer
45	687.5	16.7	779	22	AAE95610	Human protein sequ

Search completed: January 7, 2004, 20:49:51
Job time : 41.0703 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Comugen Ltd.

OM protein - protein search, using sw model

Run on: January 7, 2004, 20:54:13 ; Search time 29.7941 Seconds
(without alignments)
6851.332 Million cell updates/sec

Title: US-10-014-269-3
Perfect score: 5304
Sequence: 1 MCSQAFQAGRSQVLELVLS.....NTPSLEEDYKGRDPTLL 1013

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747907 seqs, 201509753 residues

Total number of hits satisfying chosen parameters: 747907

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA.*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCONB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PC1_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCONB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PC1US_PUBCONB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCONB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCONB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCONB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCONB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCONB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCONB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCONB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCONB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
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1	5304	100.0	1013	12	US-10-014-506-3	Sequence 3, Appl
2	5304	100.0	1013	14	US-10-014-269-3	Sequence 3, Appl
3	5304	100.0	100.0	13	US-10-002-974-3	Sequence 3, Appl
4	5304	100.0	1040	12	US-10-002-974-63	Sequence 2, Appl
5	5304	100.0	1040	14	US-10-014-506-2	Sequence 2, Appl
6	5304	100.0	1040	14	US-10-014-269-2	Sequence 2, Appl
7	5303	100.0	1040	14	US-10-002-974-62	Sequence 2, Appl
8	5301	99.9	1040	14	US-10-002-974-67	Sequence 67, Appl
9	5300	99.9	1040	14	US-10-002-974-63	Sequence 67, Appl
10	5299	99.9	1040	12	US-10-002-974-69	Sequence 69, Appl
11	5299	99.9	1040	14	US-10-014-506-4	Sequence 4, Appl
12	5299	99.9	1040	14	US-10-002-974-4	Sequence 4, Appl
13	5299	99.9	1040	14	US-10-002-974-65	Sequence 65, Appl
14	5296	99.8	1040	12	US-10-014-506-57	Sequence 57, Appl
15	5296	99.8	1040	14	US-10-002-974-57	Sequence 57, Appl
16	5296	99.8	1040	14	US-10-002-974-59	Sequence 59, Appl
17	5296	99.8	1040	14	US-10-002-974-61	Sequence 61, Appl
18	5291	99.8	1041	12	US-10-020-046A-2	Sequence 2, Appl
19	5288	99.7	1040	14	US-10-002-974-87	Sequence 87, Appl
20	5288	99.7	1040	12	US-10-014-506-55	Sequence 55, Appl
21	5288	99.7	1040	12	US-10-014-506-61	Sequence 61, Appl
22	5288	99.7	1040	14	US-10-002-974-85	Sequence 85, Appl
23	5288	99.7	1040	14	US-10-002-974-89	Sequence 89, Appl
24	5128	96.7	1007	12	US-10-014-506-34	Sequence 34, Appl
25	5128	96.7	1007	14	US-10-014-269-34	Sequence 34, Appl
26	5120	96.5	1007	14	US-10-002-974-34	Sequence 34, Appl
27	5120	96.5	1007	12	US-10-014-506-55	Sequence 55, Appl
28	5120	96.5	1007	14	US-10-002-974-55	Sequence 55, Appl
29	4980.5	93.9	1009	10	US-09-864-921-107	Sequence 107, App
30	4174	78.7	795	10	US-09-864-921-188	Sequence 188, App
31	2945	55.5	560	10	US-09-864-921-176	Sequence 176, App
32	2087	39.3	403	10	US-09-864-921-176	Sequence 176, App
33	1614	30.4	305	12	US-10-014-506-7	Sequence 7, Appl
34	1614	30.4	305	14	US-10-014-269-7	Sequence 7, Appl
35	1614	30.4	305	10	US-09-864-921-174	Sequence 174, App
36	1564	29.5	296	10	US-09-864-921-174	Sequence 174, App
37	1219.5	23.0	953	9	US-09-728-721-43	Sequence 43, Appl
38	1219.5	23.0	953	14	US-10-118-984-43	Sequence 43, Appl
39	1219.5	23.0	953	15	US-10-295-981-43	Sequence 43, Appl
40	1209.5	22.8	953	9	US-09-728-721-8	Sequence 8, Appl
41	1209.5	22.8	953	12	US-10-028-374-4	Sequence 4, Appl
42	1209.5	22.8	953	12	US-10-183-770-4	Sequence 4, Appl
43	1209.5	22.8	953	14	US-10-105-931-8	Sequence 8, Appl
44	1209.5	22.8	953	14	US-10-118-984-8	Sequence 8, Appl
45	1209.5	22.8	953	15	US-10-013-477-12	Sequence 12, Appl

Search completed: January 7, 2004, 21:06:00
Job time : 33.7941 secs

OM protein - protein search, using sw model

Run on: January 7, 2004, 20:49:58 ; Search time 16.8633 Seconds

(without alignments)
5770.121 Million cell updates/sec

Title: US-10-014-269-3

Perfect score: 5304

Sequence: 1 MCSQAFQAGRSQVLLVLS.....NPFSLSEVDKLGCRDTRLL 1013

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 263308 seqs, 9616662 residues

Total number of hits satisfying chosen parameters: 263308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR.76:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Match	Length	DB	ID	Description
No.							
1	408	7.7	1130	2	A48843		MHC class II trans
2	393.5	7.4	1192	2	T17235		hypothetical prote
3	369.5	6.9	1111	2	A59000		mater protein (imp
4	236.5	4.9	456	2	A31857		ribonuclease-inhib
5	237.5	4.5	461	2	A31858		ribonuclease-angio
6	227	4.3	456	2	S20597		ribonuclease-inhib
7	221.5	4.2	535	2	T48102		RAV GTPase activat
8	221	4.2	789	2	T52067		hypothetical prote
9	217	4.1	533	2	T52063		ran GTPase-activat
10	213	4.0	506	2	A45841		T-complex-associat
11	212.5	4.0	631	2	C89243		protein F28C1.3 (i
12	212.5	4.0	631	2	T21471		hypothetical prote
13	210	4.0	1075	2	T31668		hypothetical prote

14	209.5	3.9	545	2	T52068		RAV GTPase-activat
15	207	3.9	1004	2	T31665		hypothetical prote
16	191.5	3.6	1010	2	T36383		probable large ATP
17	191.5	3.6	1447	2	T42628		neuronal apoptosis
18	184.5	3.5	483	2	S27890		Nasopressin recept
19	173.5	3.3	862	2	T36380		probable large ATP
20	162.5	3.1	332	2	T52069		GTPase-activating
21	160	3.0	1232	2	A55478		neuronal apoptosis
22	157.5	3.0	1096	2	A96607		protein disease re
23	156.5	3.0	1119	2	A82239		hypothetical prote
24	155.5	2.9	998	2	T23427		hypothetical prote
25	155	2.9	1411	2	S44370		C2584.3 protein -
26	153.5	2.9	1121	2	T02764		myosin-I binding p
27	150.5	2.8	312	2	B97746		hypothetical prote
28	144.5	2.7	861	2	T36381		probable large ATP
29	144	2.7	662	2	S42799		garp precursor - h
30	143.5	2.7	587	2	UC5300		Ran GTPase activat
31	137	2.6	589	2	T52070		RN1 protein homol
32	136	2.6	589	2	A36983		RN1 homolog fugu
33	134	2.5	183	2	F97803		hypothetical prote
34	130	2.5	618	2	T48193		hypothetical prote
35	130	2.5	1223	2	E88451		protein K10D2.1 (i
36	129	2.4	1232	2	T05322		hypothetical prote
37	128.5	2.4	386	2	S37691		ran GTPase activat
38	127.5	2.4	603	2	UC6128		insulin-like growt
39	126.5	2.4	1547	2	A12043		hypothetical prote
40	125.5	2.4	849	2	C97303		hypothetical prote
41	125.5	2.4	1286	2	AB2042		hypothetical prote
42	124.5	2.3	800	2	AB1129		intercalin A (limp
43	124.5	2.3	1088	2	E86312		troponin - hum
44	124	2.3	359	1	A42336		hypothetical prote
45	123.5	2.3	381	2	T43444		hypothetical prote

Search completed: January 7, 2004, 20:50:42
Job time : 16.2356 secs

GenScore version 5.1.6
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OW protein - protein search, using sw model

Run on: January 7, 2004, 20:45:37; Search time 33.7667 Seconds
(without alignments)
7741.578 Million cell updates/sec

Title: US-10-014-269-3

Perfect score: 5304
Sequence: 1 MCSQEAFAQARSQLVELLS.....NTFSLEVDKLCGRPTNLL 1013

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 630525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

SPRENEL_23:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_plant:
10: sp_rodent:
11: sp_virus:
12: sp_virus:
13: sp_virus:
14: sp_virus:
15: sp_virus:
16: sp_virus:
17: sp_virus:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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1	4185	78.9	1020	11	Q8K320	Q8K320 mus musculus
2	1222.5	23.0	953	11	Q8BHB0	Q8BHB0 mus musculus
3	1209.5	22.8	953	11	Q8BWF5	Q8BWF5 homo sapien
4	1019	19.2	706	11	Q8BUT6	Q8BUT6 mus musculus
5	496	9.4	1033	11	Q8B4B8	Q8B4B8 mus musculus
6	479.5	9.0	992	4	Q8NEU4	Q8NEU4 mus musculus
7	425	8.0	1133	7	Q9G3E0	Q9G3E0 mus musculus
8	405.5	7.6	1153	7	Q9TPP1	Q9TPP1 mus musculus
9	401	7.6	1052	7	Q8NF48	Q8NF48 mus musculus
10	401	7.6	1073	7	Q9G3D8	Q9G3D8 mus musculus
11	377.5	7.1	713	6	Q9S1Z7	Q9S1Z7 mus musculus
12	377.5	6.8	409	4	Q8TFL3	Q8TFL3 mus musculus
13	362.5	6.8	982	11	Q8B4F0	Q8B4F0 mus musculus
14	360.5	6.8	982	11	Q8B4F0	Q8B4F0 mus musculus
15	357.5	6.7	733	4	Q8TEE2	Q8TEE2 mus musculus
16	344.5	6.5	1056	4	Q8NF42	Q8NF42 mus musculus
17	332	6.3	846	4	Q8IXT0	Q8IXT0 mus musculus
18	321	6.1	692	4	Q96D51	Q96D51 mus musculus
19	316.5	6.0	660	4	Q8NF06	Q8NF06 mus musculus
20	314	5.9	863	11	Q8C6J9	Q8C6J9 mus musculus
21	305	5.8	397	11	Q8B4F4	Q8B4F4 mus musculus
22	297	5.6	894	7	Q29675	Q29675 mus musculus
23	297	5.6	932	4	Q96K14	Q96K14 mus musculus
24	296.5	5.6	977	7	Q8HW99	Q8HW99 mus musculus
25	293	5.5	312	11	Q8BV65	Q8BV65 mus musculus
26	293	5.5	1097	4	Q9HEV0	Q9HEV0 mus musculus
27	284	5.4	223	4	Q8N102	Q8N102 mus musculus
28	278	5.2	605	10	Q93ZV8	Q93ZV8 mus musculus
29	273	5.1	195	4	Q8N101	Q8N101 mus musculus
30	255	4.8	748	11	Q99M00	Q99M00 mus musculus
31	250.5	4.7	817	5	Q964V6	Q964V6 mus musculus
32	245.5	4.6	310	11	Q8BYL7	Q8BYL7 mus musculus
33	243.5	4.6	620	16	Q8XZ99	Q8XZ99 mus musculus
34	239.5	4.5	554	4	Q8H7Z4	Q8H7Z4 mus musculus
35	238.5	4.5	461	4	Q8I7X3	Q8I7X3 mus musculus
36	238	4.5	1787	10	Q9V4X9	Q9V4X9 mus musculus
37	237.5	4.5	447	4	Q966D7	Q966D7 mus musculus
38	237.5	4.5	461	6	Q8H2P9	Q8H2P9 mus musculus
39	236.5	4.5	461	4	Q9B080	Q9B080 mus musculus
40	234.5	4.4	519	11	Q8C249	Q8C249 mus musculus
41	232.5	4.4	825	11	Q8C6M5	Q8C6M5 mus musculus
42	232	4.4	753	4	Q969L7	Q969L7 mus musculus
43	231.5	4.4	681	10	Q9X1K2	Q9X1K2 mus musculus
44	226.5	4.3	673	11	Q8C0N1	Q8C0N1 mus musculus
45	224	4.2	456	11	Q924P4	Q924P4 mus musculus

ALIGNMENTS

RESULT 1
Q8K320 ID Q8K320 PRELIMINARY: PRT: 1020 AA.
AC Q8K320:
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE CARD15.
GN CARD15.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Imanaga Y., Davey M.P., Martin T.M., Planck S.R., DePriest M.L.,
RA Baugh N.M., Suing C., Rosenbaum J.T.;
RT "Cloning, sequencing and expression analysis of the murine Mod2/Card15
RT gene.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF520774; AAY76073.1; -
DR MGI; MGI:2429397; Card15.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR007091; LRR_N1n1h.
DR InterPro; IPR007111; NACHT_NTPase.
DR InterPro; IPR001130; TAD_DNase.
DR PROSITE; PS50209; CARD; 2.
DR PROSITE; PS50503; LRR_R1; 1.
DR PROSITE; PS50837; NACHT; 1.
DR PROSITE; PS0137; TAD; 1.
SQ SEQUENCE 1020 AA; 113961 MW; 25504905ECF70EBB CRC64;
Query Match 78.9%; Score 4185; DB 11; Length 1020;
Best Local Similarity 79.3%; Pred. No. 0;
Matches 803; Conservative 82; Mismatches 128; Indels 0; Gaps 0;
QY 1 MCSQAFQARQSDVVELVSSLEGFEVYLWILSWELWEDYEGFHLLQQLSHLARR 60
DB 8 MCSQDEFQARQSDVALLISGLEFESILWILSWELWEDYEGFHLLQQLSHSARR 67
QY 61 LLDVTWNGTWACQKLIAAAGEAQAQSDSPKLGQWDPHSIHPARDLQSHRPAIVRLHS 120
DB 68 LLDVTWNGTWACQKLIAAAGEAQAQSDSPKLGQWDPHSIHPARDLQSHRPAIVRLHS 127
QY 121 HVENMLDLWERNGVSYQECDEIRLPITPSQARRLDLATVYKANGLAFLQHVQELP 180
DB 128 HVENMLDLWERNGVSYQECDEIRLPITPSQARRLDLATVYKANGLAFLQHVREL 187
QY 181 VPLALPLEAATCKRMKAKRTVYSAQSRELSYDGAETLCEDEITYENVLEWADVMAG 240
DB 188 APLPLPYEABQCKRTSKLRMYLQSRFLSYDSENLCEDEITYENVLELQTEVGTAG 247
QY 241 PPKSPATLGLLELSTPGHLNDADTVLVVGEAGSGKSTLLQRLHLLMAAGDPQELF 300
DB 248 ALQKSPALGLLELDFDTHLNDRDPTLVVGEAGSGKSTLLQRLHLLMATGSRFQELF 307
QY 301 VEPFSCRLQCAKPLSVRTLLFEHCQWPDVQEDIFQLLLDHPDKVLLTFDGFDEFKR 360
DB 308 IFPFCRLQCAKPLSVRTLLFEHCQWPDVQEDIFQLLLDHPDKVLLTFDGFDEFKR 367
QY 361 FTDERHCSPDPTSVQTLFNLLQGLNKAARVYTSRPAVSALFKRYITFEELKGF 420
DB 368 FTDERHCSPDPTSVQTLFNLLQGLNKAARVYTSRPAVSALFKRYITFEELKGF 427

QY 421 SEQGEILYLRKRHREPVADRLRLIDQETSLAGLCHLPVSWWVSKCHQELLQEGGSP 480
DB 428 SEQGEILYLRKRHREPVADRLRLIDQETSLAGLCHLPVSWWVSKCHQELLQEGGSP 487
QY 481 KTTDMYLLILQFLHATPPDASQSGSGLRGLPTLLHGLRLAMGLMGCCVESA 540
DB 488 TSTDMYLLILQFLHATPPDASQSGSGLRGLPTLLHGLRLAMGLMGCCVESA 547
QY 541 QQLQAQVSPDDISGLFVRAKGVPGSTAPLEFHTFQCFPAFYALISADVPPALLR 600
DB 548 QQLQAQVSPDDISGLFVRAKGVPGSTAPLEFHTFQCFPAFYALISADVPPALLR 607
QY 601 HLEFGRGSPPAALLPTVCTQASQSGSVALLQVAPENHLQTTAFLAGLSREHW 660
DB 608 HLEFGRGSPPAALLPTVCTQASQSGSVALLQVAPENHLQTTAFLAGLSREHW 667
QY 661 GLLAEQTSKALLRQACARWCLARSLRKHFSIPPAVGEAKSVHAPGFTWLRSLY 720
DB 668 DILAQCVSERVILQRQARRASTLHSHREHFSIPPAVGEAKSVHAPGFTWLRSLY 727
QY 721 EQGBRLARQARGLNVGHKLTFCVGPTECAALAFYQLHRRPVALLQIDVNSVGDIGV 780
DB 728 EQGBRLARQARGLNVGHKLTFCVGPTECAALAFYQLHRRPVALLQIDVNSVGDIGV 787
QY 781 EQLEPCGVCKALYLRNNISDRGICKLEICAHCEQQLKALFNKKITDCAHSKALL 840
DB 788 EQLEPCGVCKALYLRNNISDRGICKLEICAHCEQQLKALFNKKITDCAHSKALL 847
QY 841 ACRQFLALRLANNITPAAGQVLAESRGNTSLQFLGFVGNVGEQAQLAFLAGHQ 900
DB 848 ACRQFLALRLANNITPAAGQVLAESRGNTSLQFLGFVGNVGEQAQLAFLAGHQ 907
QY 901 SLRMLSLVGNIGSVGAQALATLAKNMLBELCEENHLQDEGVCSLAEGLKNSSLKT 960
DB 908 SLRMLSLVGNIGSVGAQALATLAKNMLBELCEENHLQDEGVCSLAEGLKNSSLKT 967
QY 961 LKLSNNGITYLGAELQALERNDDILEWLRGNFSLIEVDKLCGRDTRILL 1013
DB 968 LKLSNNGITYLGAELQALERNDDILEWLRGNFSLIEVDKLCGRDTRILL 1020
Search completed: January 7, 2004, 20:52:36
Job time : 37.7667 secs

and is derived by analysis of the total score distribution.

SOMPARIES

OM protein - protein search, using sw model

Run on: January 7, 2004, 20:04:17 ; Search time 39.085 seconds

(without alignments)
4223.507 Million cell updates/sec

Title: US-10-014-269-2

Perfect score: 5448

Sequence: 1 MGEEGASAHDEBRASVLL.....NTFSLEVDKGRDFRLL 1040

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A.Geneseq.19Jun03:*

1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1960.DAT:*

2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1961.DAT:*

3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1962.DAT:*

4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1963.DAT:*

5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1964.DAT:*

6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1965.DAT:*

7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1966.DAT:*

8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1967.DAT:*

9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1968.DAT:*

10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1969.DAT:*

11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1970.DAT:*

12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1971.DAT:*

13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1972.DAT:*

14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1973.DAT:*

15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1974.DAT:*

16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1975.DAT:*

17: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1976.DAT:*

18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1977.DAT:*

19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1978.DAT:*

20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1979.DAT:*

21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*

22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*

23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*

24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.

Result No.	Score	Query		DB ID	Description
		Match	Length		
1	5448	100.0	1040	23	Human No22 protein
2	5447	100.0	1040	23	Human No22 protein
3	5445	99.9	1040	23	Human No22 protein
4	5444	99.9	1040	23	Human No22 protein
5	5443	99.9	1040	23	Human No22 protein
6	5443	99.9	1040	23	Human No22 protein
7	5443	99.9	1040	23	Human No22 protein
8	5440	99.9	1040	23	Human No22 protein
9	5440	99.9	1040	23	Human No22 protein
10	5440	99.9	1040	23	Human No22 protein
11	5440	99.9	1040	23	Human No22 protein
12	5435	99.8	1040	23	Human No22 protein
13	5432	99.7	1040	23	Human No22 protein
14	5432	99.7	1040	23	Human No22 protein
15	5331	97.9	1041	22	Human No22 protein
16	5304	97.4	1013	23	Human No22 protein
17	5304	97.4	1013	23	Human No22 protein
18	5272	96.8	1007	23	Human No22 protein
19	5272	96.8	1007	23	Human No22 protein
20	5264	96.6	1007	23	Human No22 protein
21	4994.5	91.7	1009	23	Human No22 protein
22	4188	76.9	793	23	Human No22 protein
23	2959	54.3	560	23	Human No22 protein
24	2087	38.3	403	23	Human No22 protein
25	1614	29.6	305	23	Human No22 protein
26	1614	29.6	305	23	Human No22 protein
27	1564	28.7	296	23	Human No22 protein
28	1219.5	22.4	953	20	Human No22 protein
29	1219.5	22.4	953	22	Human No22 protein
30	1219.5	22.4	953	23	Human No22 protein
31	1219.5	22.4	953	23	Human No22 protein
32	1219.5	22.4	953	24	Human No22 protein
33	1212	22.2	953	22	Human No22 protein
34	1209.5	22.2	953	21	Human No22 protein
35	1209.5	22.2	953	22	Human No22 protein
36	1209.5	22.2	953	22	Human No22 protein
37	1209.5	22.2	953	23	Human No22 protein
38	1209.5	22.2	953	24	Human No22 protein
39	1208.5	22.1	953	23	Human No22 protein
40	1204.5	22.1	953	20	Human No22 protein
41	1171	21.5	966	24	Human No22 protein
42	1001	18.4	705	21	Human No22 protein
43	1001	18.4	705	21	Human No22 protein
44	1001	18.4	719	22	Human No22 protein
45	887.5	16.3	779	22	Human No22 protein

Search completed: January 7, 2004, 20:49:48
Job time : 43.085 secs

GenCore version 5.1.6
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OK protein - protein search, using sw model

Run on: January 7, 2004, 20:54:13 : Search time 30.5882 Seconds

(without alignments)
6831.332 Million cell updates/sec

Title: US-10-014-269-2

Perfect score: 5448

Sequence: 1 MEEEGGASHDEERASVLL.....NTFSLEWDYLGCRDRLLL 1040

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747907 seqs, 201509753 residues

Total number of hits satisfying chosen parameters: 747907

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications, AA:*

1: /cgn2_6/p/odata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/p/odata/2/pubpaa/PCU_NEW_PUB.pep:*
3: /cgn2_6/p/odata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/p/odata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/p/odata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/p/odata/2/pubpaa/PCUS_PUBCOMB.pep:*
7: /cgn2_6/p/odata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/p/odata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/p/odata/2/pubpaa/US09_PUBCOMB.pep:*
10: /cgn2_6/p/odata/2/pubpaa/US09C_PUBCOMB.pep:*
11: /cgn2_6/p/odata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/p/odata/2/pubpaa/US09C_PUBCOMB.pep:*
13: /cgn2_6/p/odata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/p/odata/2/pubpaa/US10C_PUBCOMB.pep:*
15: /cgn2_6/p/odata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/p/odata/2/pubpaa/US10C_PUBCOMB.pep:*
17: /cgn2_6/p/odata/2/pubpaa/US10C_PUBCOMB.pep:*
18: /cgn2_6/p/odata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
------------	-------	-------------	--------	----	-------------

Search completed: January 7, 2004, 21:05:56
Job time : 33.5882 secs

1	5448	100.0	1040	12	US-10-014-269-2	Sequence 2, Appl
2	5448	100.0	1040	14	US-10-014-269-2	Sequence 2, Appl
3	5448	100.0	1040	14	US-10-002-974-2	Sequence 2, Appl
4	5447	100.0	1040	14	US-10-002-974-2	Sequence 67, Appl
5	5445	99.9	1040	14	US-10-002-974-63	Sequence 63, Appl
6	5444	99.9	1040	14	US-10-002-974-63	Sequence 69, Appl
7	5443	99.9	1040	12	US-10-002-974-68	Sequence 4, Appl
8	5443	99.9	1040	14	US-10-014-269-4	Sequence 4, Appl
9	5443	99.9	1040	14	US-10-002-974-4	Sequence 4, Appl
10	5443	99.9	1040	12	US-10-002-974-65	Sequence 65, Appl
11	5440	99.9	1040	12	US-10-014-506-57	Sequence 57, Appl
12	5440	99.9	1040	14	US-10-002-974-57	Sequence 57, Appl
13	5440	99.9	1040	14	US-10-002-974-59	Sequence 59, Appl
14	5440	99.9	1040	14	US-10-002-974-61	Sequence 61, Appl
15	5435	99.8	1040	14	US-10-002-974-67	Sequence 87, Appl
16	5432	99.7	1040	12	US-10-014-506-59	Sequence 59, Appl
17	5432	99.7	1040	12	US-10-014-506-61	Sequence 61, Appl
18	5432	99.7	1040	14	US-10-002-974-85	Sequence 85, Appl
19	5432	99.7	1040	14	US-10-002-974-89	Sequence 89, Appl
20	5331	97.9	1041	12	US-10-240-044A-2	Sequence 2, Appl
21	5304	97.4	1043	12	US-10-014-506-3	Sequence 3, Appl
22	5304	97.4	1043	14	US-10-014-269-3	Sequence 3, Appl
23	5304	97.4	1043	14	US-10-002-974-3	Sequence 3, Appl
24	5272	96.8	1007	12	US-10-014-506-34	Sequence 34, Appl
25	5272	96.8	1007	14	US-10-014-269-34	Sequence 34, Appl
26	5272	96.8	1007	14	US-10-002-974-34	Sequence 34, Appl
27	5264	96.6	1007	12	US-10-014-506-55	Sequence 55, Appl
28	5264	96.6	1007	14	US-10-002-974-55	Sequence 55, Appl
29	4994.3	91.7	1009	10	US-09-864-921-107	Sequence 107, App
30	4188	76.9	795	10	US-09-864-921-188	Sequence 188, App
31	2959	54.3	560	10	US-09-864-921-83	Sequence 83, Appl
32	2087	38.3	403	10	US-09-864-921-176	Sequence 176, App
33	1614	28.6	305	12	US-10-014-269-7	Sequence 7, Appl
34	1614	28.6	305	14	US-10-014-506-7	Sequence 7, Appl
35	1614	28.6	305	14	US-10-002-974-7	Sequence 7, Appl
36	1564	28.7	296	10	US-09-864-921-174	Sequence 174, App
37	1219.5	22.4	953	9	US-09-728-721-43	Sequence 43, Appl
38	1219.5	22.4	953	14	US-10-118-984-43	Sequence 43, Appl
39	1219.5	22.4	953	15	US-10-295-981-43	Sequence 43, Appl
40	1209.5	22.2	953	9	US-09-728-721-8	Sequence 8, Appl
41	1209.5	22.2	953	12	US-10-028-374-4	Sequence 4, Appl
42	1209.5	22.2	953	12	US-10-183-770-4	Sequence 4, Appl
43	1209.5	22.2	953	14	US-10-105-931-8	Sequence 8, Appl
44	1209.5	22.2	953	14	US-10-118-984-8	Sequence 8, Appl
45	1209.5	22.2	953	15	US-10-013-477-12	Sequence 12, Appl

OK protein - protein search, using sw model

Run on: January 7, 2004, 20:49:58 ; Search time 17.333 Seconds

(without alignments)
5770.121 Million cell updates/sec

Title: US-10-014-269-2

Perfect score: 5448

Sequence: 1 MGEEGSSASIDEERASVLT.....NTPSLEVDKLGCRDTRL 1040

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1.*
2: p1r2.*
3: p1r3.*
4: p1r4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Match	Length	DB	ID	Description
No.							
1	408	7.5	1130	2	A48843		MHC class II trans
2	393.5	7.2	1192	2	T11735		hypothetical prote
3	363.5	6.7	1111	2	A59000		matern protein (imp
4	258.5	4.7	456	2	A31657		ribonuclease-inhib
5	237.5	4.4	461	2	A31658		ribonuclease-angio
6	227	4.2	456	2	S20597		ribonuclease-inhib
7	221.5	4.1	535	2	T48102		RAN GTPase activat
8	221	4.1	789	2	T52067		hypothetical prote
9	217	4.0	553	2	T52063		RAN GTPase-activat
10	213	3.9	506	2	A45841		T-complex-associat
11	212.5	3.9	631	2	C89243		protein F28C1.3 [i
12	212.5	3.9	631	2	T21471		hypothetical prote
13	210	3.9	1075	2	T31668		hypothetical prote

14	209.5	3.8	545	2	T52068		RAN GTPase-activat
15	207	3.8	1004	2	T31665		hypothetical prote
16	196	3.6	1447	2	T42628		neuronal apoptosis
17	191.5	3.5	1010	2	T36383		probable large ATP
18	184.5	3.4	483	2	S27880		Nasopressin recept
19	173.5	3.2	862	2	T36380		probable large ATP
20	162.5	3.0	332	2	T52069		GTPase-activating
21	160	2.9	1232	2	A55478		neuronal apoptosis
22	157.5	2.9	1096	2	A96607		protein disease re
23	156.5	2.9	1119	2	AB2239		hypothetical prote
24	155.5	2.9	998	2	T23427		hypothetical prote
25	155	2.8	1411	2	S44770		C29e4.3 protein -
26	153.5	2.8	1121	2	T02764		myosin-I binding p
27	150.5	2.8	312	2	B97746		hypothetical prote
28	144.5	2.7	861	2	T36381		probable large ATP
29	144	2.6	662	2	S42799		garp precursor - h
30	143.5	2.6	587	2	UC5300		RAN GTPase activat
31	137	2.5	589	2	T52070		RAN protein homol
32	136	2.5	589	2	A36583		RAN homolog fugu
33	134	2.5	183	2	F97803		hypothetical prote
34	130	2.4	618	2	T48193		hypothetical prote
35	130	2.4	1223	2	E88451		protein K10D2.1 [i
36	129	2.4	1232	2	T05322		hypothetical prote
37	128.5	2.4	386	2	S37691		insulin-like growt
38	127.5	2.3	603	2	UC6128		hypothetical prote
39	126.5	2.3	1547	2	A12043		hypothetical prote
40	125.5	2.3	849	2	C97803		hypothetical prote
41	125.5	2.3	1256	2	AB2042		hypothetical prote
42	124.5	2.3	800	2	AB1129		interleukin A (limp
43	124.5	2.3	1088	1	E86312		Flt1A6.9 protein -
44	124	2.3	359	1	A42336		tropomodulin - hum
45	124	2.3	1151	2	T30936		reverse transcript

Search completed: January 7, 2004, 20:50:37
Job time : 16.5556 secs

OM protein - protein search, using sw model

Run on: January 7, 2004, 20:45:37 ; Search time 34.6667 Seconds
(without alignments)
7741.578 Million cell updates/sec

Title: US-10-014-269-2

Perfect score: 5448

Sequence: 1 MGSEGGASHDEERASVLL.....NFSLEEVKLCGRDRLLL 1040

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08

Maximum Match 1008

Listing first 45 summaries

Database :

1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP virus:*
16: SP bacteriophage:*
17: SP archaea:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
------------	-------	-------------	--------	----	-------------

1	4195	77.0	1020	11	Q8K320	Q8K320 mus musculus
2	1222.5	22.4	953	11	Q8B80	Q8B80 mus musculus
3	1209.5	22.2	953	11	Q8B80	Q8B80 mus musculus
4	1019	18.7	706	11	Q8B80	Q8B80 mus musculus
5	496	9.1	1033	11	Q8B48	Q8B48 mus musculus
6	479.5	8.8	892	4	Q8NEU4	Q8NEU4 mus musculus
7	425	7.8	1153	7	Q8GJEO	Q8GJEO mus musculus
8	425	7.8	1155	7	Q8GJEP1	Q8GJEP1 mus musculus
9	405.5	7.4	1778	4	Q8NF48	Q8NF48 mus musculus
10	401	7.4	1032	7	Q8GJED	Q8GJED mus musculus
11	401	7.4	1073	7	Q8GJED9	Q8GJED9 mus musculus
12	377.5	6.9	713	6	Q8S1Z7	Q8S1Z7 mus musculus
13	362.5	6.7	499	4	Q8RT13	Q8RT13 mus musculus
14	360.5	6.6	982	11	Q8BU40	Q8BU40 mus musculus
15	357.5	6.6	733	4	Q8TEE2	Q8TEE2 mus musculus
16	344.5	6.3	1056	4	Q8N442	Q8N442 mus musculus
17	332	6.1	846	4	Q8IXT0	Q8IXT0 mus musculus
18	321	5.9	692	4	Q8ND51	Q8ND51 mus musculus
19	316.5	5.8	660	4	Q8NE06	Q8NE06 mus musculus
20	314	5.8	863	11	Q8C639	Q8C639 mus musculus
21	305	5.6	397	11	Q8B9F4	Q8B9F4 mus musculus
22	297	5.5	884	7	Q26675	Q26675 mus musculus
23	297	5.5	932	4	Q8K6L4	Q8K6L4 mus musculus
24	296.5	5.4	977	7	Q8HW99	Q8HW99 mus musculus
25	293	5.4	312	11	Q8BV65	Q8BV65 mus musculus
26	293	5.4	1097	4	Q8HY60	Q8HY60 mus musculus
27	284	5.2	223	4	Q8N102	Q8N102 mus musculus
28	278	5.1	605	10	Q93ZV8	Q93ZV8 mus musculus
29	273	5.0	195	4	Q8N101	Q8N101 mus musculus
30	255	4.7	748	11	Q99M60	Q99M60 mus musculus
31	250.5	4.6	817	5	Q964V6	Q964V6 mus musculus
32	245.5	4.5	310	11	Q8BYL7	Q8BYL7 mus musculus
33	243.5	4.5	620	16	Q8XZ99	Q8XZ99 mus musculus
34	239.5	4.4	554	4	Q8H724	Q8H724 mus musculus
35	238.5	4.4	461	4	Q8ITX8	Q8ITX8 mus musculus
36	238	4.4	1787	10	Q8W4X9	Q8W4X9 mus musculus
37	237.5	4.4	447	4	Q8G6D7	Q8G6D7 mus musculus
38	237.5	4.4	461	6	Q8H2P9	Q8H2P9 mus musculus
39	236.5	4.3	461	4	Q8B080	Q8B080 mus musculus
40	234.5	4.3	519	11	Q8C249	Q8C249 mus musculus
41	232.5	4.3	825	11	Q8C6M5	Q8C6M5 mus musculus
42	232	4.3	753	4	Q8G6L7	Q8G6L7 mus musculus
43	231.5	4.2	681	10	Q8Y1X2	Q8Y1X2 mus musculus
44	229	4.2	1403	11	Q8CH64	Q8CH64 mus musculus
45	228	4.2	1403	11	Q8CH68	Q8CH68 mus musculus

ALIGNMENTS

RESULT 1
ID Q8K320 PRELIMINARY: PRT: 1020 AA.
AC Q8K320,
DT 01-OCT-2002 (TRENDSrel. 22, Created)
DT 01-OCT-2002 (TRENDSrel. 22, Last sequence update)
DT 01-MAR-2003 (TRENDSrel. 23, Last annotation update).

DE CARD5.
 GN Mus musculus (House).
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RA Tanaka T., Davey M.P., Martin T.M., Planck S.R., Defriest M.L.,
 RA Baugh M.M., Suling C., Rosenbaum J.T.;
 RT "Cloning, sequencing and expression analysis of the murine Nod2/Card15
 gene";
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF520774; AA076073.1;
 DR MGI; MGI:2429397; Card15.
 DR InterPro; IPR001315; CARD.
 DR InterPro; IPR007091; LRR_RNinh.
 DR InterPro; IPR007111; NACHT_NTPase.
 DR InterPro; IPR001301; IatD_DNase.
 DR PROSITE; PS50209; CARD_2.
 DR PROSITE; PS50503; LRR_Rif_1.
 DR PROSITE; PS50837; NACHT_1.
 DR PROSITE; PS01137; TATD_1.
 DR PROSITE; PS01137; TATD_1.
 SQ SEQUENCE 1020 AA; 11361 MM; 2504905 ECF70FBB CRC64;

Query Match 77.0%; Score 4196; DB 11; Length 1020;
 Best Local Similarity 79.2%; Pred. No. 0;
 Matches 804; Conservative 83; Mismatches 128; Indels 0; Gaps 0;

QY 26 CEMCQEAFOAQSQVLELVSSGLDGEFESVLDKLSWESVSWEDYEGHLLGQPLSHLA 85
 DB 6 CDMCQEEFQAQSSQLVALLSSLEGEESTLMDLMSVDVLSREDEYGLSPGQPLSHSA 65
 QY 86 RLIDTWNKGTWACQKTLAAQEAQADQSPKLGCMQDPHSILHPPARDIOSHPATVRL 145
 DB 66 RLIDTWNKGTWACQKTLAAQEAQADQSPKLGCMQDPHSILHPPARDIOSHPATVRL 125
 QY 146 HSHVENMLDLAMERGVSYQECDEIRLPIFTPSQARRLLDLATVANGLAFLQWQE 205
 DB 126 YNHEPMKELAREGFLSYQECDEIRLPIFTPSQARRLLDLAAVANGLAFLQWQE 185
 QY 206 LPVPLALPLEATCKRYAKLRTTVAQSRFTSYDGAETICLEDIYENLVEMADVM 265
 DB 186 LPAPLPLEYBAECQKFTSKRTMTLQSRFTSYDGSNLCLEDIYENLVEMADVM 245
 QY 266 AGPQKSPATLGLLEFSTPGHNDADTVLVYGAAGSKSTLLQRLHLLMAAGQDFEF 325
 DB 246 AGALQKSPAILGLLEFSTPGHNDADTVLVYGAAGSKSTLLQRLHLLMAAGQDFEF 305
 QY 326 LFVFPFCGQLOGMARPLSVRIITLFEHCQDPVQGEDIFQLLDHPRVLLTFDGFDEF 385
 DB 306 LFVFPFCGQLOGMARPLSVRIITLFEHCQDPVQGEDIFQLLDHPRVLLTFDGFDEF 365
 QY 386 FRITDRHCSPTDPTSVQTLFNLQGNLKNARKVVTSPAAVSAPLRYKIRTEFLK 445
 DB 366 FRITDRHCSPTDPTSVQTLFNLQGNLKNARKVVTSPAAVSAPLRYKIRTEFLK 425

QY 446 GFSEQIEILYRKRRHEBQVADRLHLLQETSALHGLPVEFVSWWVSKQCQELLQBSG 505
 DB 426 GFSEQIEILYRKRRHEBQVADRLHLLQETSALHGLPVEFVSWWVSKQCQELLQBSG 485
 QY 506 SPRTTDMYLLIQFLHATPPDASAGLOPFLRGPLFTLHGLRLALWGLOKCYVF 565
 DB 486 SPRTTDMYLLIQFLHATPPDASAGLOPFLRGPLFTLHGLRLALWGLOKCYVF 545
 QY 566 SAQQLAAQVSPDDISLGEFVRAKGVGTAPELFTHPOCFAPAYLALASDVPRL 625
 DB 546 SAQQLAAQVSPDDISLGEFVRAKGVGTAPELFTHPOCFAPAYLALASDVPRL 605
 QY 626 LRLNLCGRPNASPARLLPNCIOASGQSSVALLQXAEPRNLQITAAFLAGLSRE 685
 DB 606 LRLNLCGRPNASPARLLPNCIOASGQSSVALLQXAEPRNLQITAAFLAGLSRE 665
 QY 686 HMGLLAECOTSEKALLRROACARWCLARKEFHSPPAAPGEAKSVHAMPFTWLR 745
 DB 666 HRLLLAQVSENVLLQKRAASCLASLREHFSIPPAVPEFTSVHAMPFTWLR 725
 QY 746 LYBQEEFLAKRAAGLVGHLKTFQSVGPTCCALAFVQLHRRPVALLDYNVSDI 805
 DB 726 LYBQEEFLAKRAAGLVGHLKTFQSVGPTCCALAFVQLHRRPVALLDYNVSDI 785
 QY 806 GVEQLLPGLQVCKALYLRDNNTSDRGICKEICQLHCEQOKLALFNKRLDGCASHAK 865
 DB 786 GVEQLLPGLQVCKALYLRDNNTSDRGICKEICQLHCEQOKLALFNKRLDGCASHAK 845
 QY 866 LLAQRNELLRLANNVITTAAGQVLAEGRGNTSLQPLTFWGNRVGDEGAQLEALGD 925
 DB 846 LLAQRNELLRLANNVITTAAGQVLAEGRGNTSLQPLTFWGNRVGDEGAQLEALGD 905
 QY 926 HQSLKSTLVANNIGSVGAQALALMLANNMLEELCBENHLQDEGVCSLAEGKRNSTL 985
 DB 906 HQSLKSTLVANNIGSVGAQALALMLANNMLEELCBENHLQDEGVCSLAEGKRNSTL 965
 QY 986 KILKLNNGITYLGAELALQALERNDITLFWLRGNTFSLSEVDKLGCRDTRILL 1040
 DB 966 KILKLNNGITYLGAELALQALERNDITLFWLRGNTFSLSEVDKLGCRDTRILL 1020

Search completed: January 7, 2004, 20:52:32
 Job time : 39.6667 secs

OK nucleic - protein search, using frame_plus_nzp model

Run on: January 7, 2004, 19:23:16 : Search time 110.738 Seconds

(without alignments)
12857.211 Million cell updates/sec

Title: US-10-014-269-1

Perfect score: 8270

Sequence: 1 gtagacagatccagctccac.....ataacgttgagtcacaaac 4485

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 2215726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Command line parameters:

-MODEL=frame+_nzp.model -DEV=xlp

Q=/gen2_1/USPRO_pool_p/US10014269/runet_07012004_175228_24497/app_query.fasta_1

.9358

-DB=A_Geneseq_19Jun03 -OPM=fastan -SUFFIX=reg -MINMATCH=0.1 -LOOPCL=0

-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsun62 -TRANS=human40.cdi

-LIST=150 -DOCALLIGN=200 -THR_SCORE=pcr -THR_MAX=100 -THR_MIN=0 -ALIGN=50

-MODE=LOCAL -OUTFMT=pro -NORW=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000

-USER=US10014269 -GCN 1.1 311 -runet_07012004_175228_24497 -NCPU=6 -ICPU=3

-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGID=0

-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6

-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELDP=6 -DELEXT=7

Database: A_Geneseq_19Jun03:*

1: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
7: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
8: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
9: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
10: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5448	65.9	1040	23	AAE23416 Human Nod2 protein
2	5447	65.9	1040	23	ABJ04773 Nod2a V9551 protei
3	5445	65.8	1040	23	ABJ04771 Nod2a V793M protei
4	5444	65.8	1040	23	ABJ04774 Nod2a N863V protei
5	5443	65.8	1040	23	AAE23418 Human Nod2 protein
6	5443	65.8	1040	23	ABJ04737 Nod2a N852S protei
7	5443	65.8	1040	23	ABJ04772 Nod2a R702W protei
8	5440	65.8	1040	23	ABJ04735 Nod2a G908R (SNP)7
9	5440	65.8	1040	23	ABJ04768 Nod2a P268S + N852
10	5440	65.8	1040	23	ABJ04769 Nod2a P268S + N852
11	5440	65.8	1040	23	ABJ04776 Nod2a P268S + R702
12	5432	65.7	1040	23	ABJ04775 Nod2a P268S + R702
13	5432	65.7	1040	23	ABJ04777 Nod2a P268S + R702
14	5432	65.7	1040	23	ABJ04778 Nod2a P268S + R702
15	5331	64.5	1041	22	AAE23417 Human Nod2 protein
16	5304	64.1	1013	23	AAE23419 Human Nod2 protein
17	5304	64.1	1013	23	ABJ04736 Nod2b protein wild
18	5272	63.7	1007	23	AAE23434 Human Nod2 mutant
19	5272	63.7	1007	23	ABJ04766 Nod2a P268S + R702
20	5264	63.7	1007	23	ABJ04767 Nod2a P268S + R702
21	4994.5	60.4	1009	23	AAU80865 Human CARD3X prote
22	4188	50.6	795	23	AAU80875 Human CARD3X prote
23	2959	35.8	560	23	AAU80886 Human CARD3X prote
24	2087	25.2	403	23	AAE23421 Human Nod2 protein
25	1614	19.5	305	23	AAE23421 Human Nod2 protein
26	1614	18.9	305	23	ABJ04740 Nod2 nucleotide bi
27	1564	18.9	296	23	AAU80869 Human CARD3X NB-NR
28	1219.5	14.7	953	20	AAV31145 Murine CARD-4L pro
29	1219.5	14.7	953	22	ABG31084 Mouse CARD-4L (lon
30	1219.5	14.7	953	23	ABG31084 Mouse caspase recr
31	1219.5	14.7	953	23	AAU22136 Protein of murine
32	1219.5	14.7	953	24	ABU6228 Mouse Caspase recr
33	1212	14.7	953	22	AAU79473 Human protein SEQ

34	1209.5	14.6	953	21	AAH15552	Apoptosis related	91	433	5.2	1130	19	AAW80313	CITF (class II tr
35	1209.5	14.6	953	22	AAH78459	Human protein SBO	92	433	5.2	1130	19	AAW57056	Class II trans act
36	1209.5	14.6	953	23	AAH20080	Human CARD-4L (lon	93	433	5.2	1207	19	AAW80311	CITF (class II tr
37	1209.5	14.6	953	24	AAO22111	Protein of human C	94	429.5	5.2	896	23	AAO15592	Human PYRIN-11 pro
38	1209.5	14.6	953	25	AAH56273	Human Caspase recr	95	425	5.1	320	23	AAH04763	Nod1 protein sequ
39	1208.5	14.6	953	26	ABG31076	Human Caspase recr	96	421.5	5.1	869	22	AAH63138	Human transcriptio
40	1204.5	14.6	953	27	AAH31141	Human CARD-4L prot	97	418	5.1	81	22	AAH08068	Human CARD3X CARDB
41	1171	14.2	966	28	AAH56300	Caspase recruitment	98	415	5.0	1454	22	AAH72673	Human NAC beta iso
42	1001	12.1	705	29	AAH15559	Apoptosis related	99	414.5	5.0	1429	23	AAH78455	Human caspase recr
43	1001	12.1	705	30	AAH15562	Fragment of apopto	100	414.5	5.0	1429	23	AAO17855	Human caspase recr
44	1001	12.1	719	31	AAH55889	Human colon cancer	101	414.5	5.0	1473	22	AAH6758	Human G-protein co
45	887.5	10.4	779	32	AAH55890	Human protein sequ	102	411.5	5.0	1473	22	AAH72674	Human G-protein co
46	858	10.4	166	33	ABG49110	Human liver peptid	103	411	5.0	830	19	AAH50314	CITF (class II tr
47	858	10.4	166	34	ABG49110	Peptide #1756 enco	104	411	5.0	1397	22	AAH72671	CITF (class II tr
48	858	10.4	166	35	ABH19702	Protein #1701 enco	105	411	5.0	1442	22	AAH72671	Human NB-NRC and C
49	858	10.4	166	36	AAH55062	Human brain expres	106	410.5	5.0	1429	22	AAH62571	Human NB-NRC and C
50	858	10.4	166	37	AAH67453	Human bone marrow	107	410.5	5.0	1429	23	AAH97969	Human CARD-7 poly
51	858	10.4	166	38	AAH03024	Peptide #1706 enco	108	410.5	5.0	1429	23	ABG74472	Human leucine rich
52	840	10.2	155	39	ABG37074	Human peptid enco	109	410.5	5.0	1429	23	ABH77916	Human leucine rich
53	840	10.2	155	40	ABG38852	Human liver peptid	110	410.5	5.0	1429	24	ABG71633	Human leucine rich
54	840	10.2	155	41	ABH43475	Peptide #10981 enco	111	410.5	5.0	1473	22	AAH72669	Human caspase recr
55	840	10.2	155	42	ABH26439	Protein #438 enco	112	410.5	5.0	1473	22	AAH72669	Human caspase recr
56	840	10.2	155	43	AAH64407	Human brain expres	113	410.5	5.0	1473	22	AAH72669	Human NB-NRC and C
57	840	10.2	155	44	AAH72225	Human bone marrow	114	408	4.9	76	23	AAH08067	Human CARD3X CARDB
58	840	10.2	155	45	AAH21157	Peptide #7591 enco	115	399.5	4.8	919	23	AAH43483	Human secreted pro
59	840	10.2	155	46	AAH37368	Peptide #11405 enco	116	399.5	4.8	919	24	AAH19319	NOVX related prote
60	840	10.2	155	47	ABG46236	Human peptid enco	117	396.5	4.8	920	23	AAH53254	Human NOD1-13 prot
61	820	9.9	146	48	ABG38853	Human liver peptid	118	396	4.8	858	23	AAH530328	Human nucleotide b
62	820	9.9	146	49	ABH43476	Peptide #10982 enco	119	396	4.8	858	23	AAH01870	Human nucleotide b
63	820	9.9	146	50	ABH26440	Protein #438 enco	120	396	4.8	994	23	AAH01593	Human PYRIN-3 prot
64	820	9.9	146	51	AAH64408	Human brain expres	121	395	4.8	952	22	ABG03924	Novel human diapo
65	820	9.9	146	52	AAH72226	Human bone marrow	122	391.5	4.7	1022	23	AAH01862	Streptomyces virid
66	820	9.9	146	53	AAH21158	Peptide #7592 enco	123	391.5	4.7	1022	23	AAH01862	Streptomyces virid
67	820	9.9	146	54	AAH37369	Peptide #11406 enco	124	390.5	4.7	1049	22	AAH65894	Human domain conta
68	820	9.9	146	55	ABG46237	Human peptid enco	125	385	4.7	860	23	AAH98224	Human CGD SEQ ID
69	652.5	7.9	180	56	AAH08076	Human CARD3X #1.	126	385	4.7	860	23	AAH98224	Human nucleotide b
70	593	7.2	140	57	AAH08077	Mouse CARD3X #2.	127	384.5	4.6	1851	22	AAH00023	Human activated T-
71	588	7.1	139	58	AAH08078	Human CARD3X #2.	128	384.5	4.6	1851	23	AAH01860	Human domain conta
72	531	6.4	1061	59	AAH01590	Human CARD-45 part	129	379.5	4.6	1062	22	AAH65895	Human domain conta
73	530.5	6.4	490	60	AAH31142	Human CARD-45 part	130	379.5	4.6	1062	23	AAH01866	Human domain conta
74	530.5	6.4	490	61	ABG31077	Human CARD-45 (sho	131	375	4.5	1033	22	AAH07856	Human nucleotide b
75	530.5	6.4	490	62	AAH22127	Human caspase recr	132	375	4.5	1033	23	AAH07856	Human nucleotide b
76	530.5	6.4	490	63	AAH56289	Protein of human C	133	375	4.5	1033	24	ABH7456	Human nucleotide b
77	530.5	6.4	490	64	AAH017857	Human CARD-45 part	134	368	4.5	1033	24	ABH7456	Human nucleotide b
78	530.5	6.4	490	65	AAH017857	Human CARD-45 part	135	368	4.5	1033	24	ABH7456	Human nucleotide b
79	522	6.3	97	66	AAH04738	Human CARD-45 (sho	136	366	4.4	740	22	ABG03831	Human G-protein co
80	522	6.3	97	67	AAH04738	Human CARD-45 (sho	137	365.5	4.4	1111	23	AAH79525	Mouse MAFK protei
81	497	6.0	1034	68	AAH080503	Human CARD-45 (sho	138	364	4.4	1344	23	AAH015585	Human CARD-45 (sho
82	497	6.0	1034	69	AAH080503	Human CARD-45 (sho	139	364	4.4	1344	23	AAH015585	Human CARD-45 (sho
83	485	5.9	94	70	AAH04739	Human CARD-45 (sho	140	360.5	4.4	19338	24	ABH76679	Human CARD-45 (sho
84	485	5.9	94	71	AAH04739	Human CARD-45 (sho	141	358.5	4.3	2312	23	AAH017859	Human CARD-45 (sho
85	442.5	5.4	975	72	AAH72596	Human CARD-45 (sho	142	357	4.3	1033	23	AAH017859	Human CARD-45 (sho
86	438.5	5.3	19938	73	AAH72596	Human CARD-45 (sho	143	357	4.3	1162	23	AAH28053	Human CARD-45 (sho
87	433	5.2	1106	74	AAH72596	Human CARD-45 (sho	144	355.5	4.3	1200	23	AAH72596	Human CARD-45 (sho
88	433	5.2	1106	75	AAH72596	Human CARD-45 (sho	145	355.5	4.3	1200	24	AAH72596	Human CARD-45 (sho
89	433	5.2	1130	76	AAH72596	Human CARD-45 (sho	146	355	4.3	19338	24	AAH72596	Human CARD-45 (sho
90	433	5.2	1130	77	AAH72596	Human CARD-45 (sho	147	352.5	4.3	19338	24	AAH72596	Human CARD-45 (sho

148 350.5 4.2 1111 24 AAF31748
c 149 348 4.2 19938 24 ABB86398
c 150 343.5 4.2 777 14 AAR37740
Mouse WATER protei
Streptomyces virid
Collagen-like poly

ALIGNMENTS

RESULT 1

ID AAE25416 standard; Protein; 1040 AA.

XX AAE25416;

DT 30-OCT-2002 (first entry)

DE Human Nod2 protein #1.

KW Human; Nod2 polypeptide; gene shuffling; transgenic plant; apoptosis;
KW Crohn's disease; antiinflammatory; gene therapy.

XX Homo sapiens.

PV W0200236773-A2.

PD 10-MAY-2002.

PF 26-OCT-2001; 2001WO-US47699.

PR 30-OCT-2000; 2000US-244289P.

PR 26-OCT-2001; 2001US-0244289.

XX (UNMT) UNIV MICHIGAN.

PI Nunez G, Itohara N, Ogura Y;

DR WPI; 2002-537300/57.

DR N-PSDB; AAD41434.

PT Novel Nod2 polypeptides and polynucleotides useful in treating diseases
PT or altering physiological states marked by apoptosis of cells or other
PT nuclear factor-kappa B mediated effects -

PS Claim 25; Fig 13; 18pp; English.

XX The invention relates to a purified Nod2 polypeptide and its
CC polynucleotide. The invention is useful for inhibiting Nod2 interaction
CC with NF-kB and its associated proteins. Nod2 polynucleotides used in
CC frame to a marker sequence is useful for purifying Nod2 polypeptide.
CC Nod2 polynucleotides are also useful in gene shuffling or sexual
CC polymerase chain reaction (PCR) procedures. Nod2 polynucleotides are
CC also useful to either increase or decrease the level of Nod2 mRNA and/or
CC protein in transfected cells as compared to the levels in wild-type cells
CC and to decrease the level of Nod2 mRNA or protein in transgenic plants,
CC plant tissues and plant cells as compared to the levels in wild-type.
CC The invention is useful for inhibiting NF-kB activity and thus for
CC treating Crohn's disease. Nod2 polypeptides and polynucleotides are
CC useful in treating diseases or altering physiological states marked by

CC apoptosis of cells or other NF-kB mediated effects. Nod2 gene is useful
CC in gene therapy. The present sequence is Nod2 protein.
XX
SQ Sequence 1040 AA;

Alignment Scores:

Pred. No.: 0 Length: 1040
Score: 5448.00 Matches: 1040
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 65.88% Indels: 0
DB: 23 Gaps: 0

US-10-014-269-1 (1-4485) x AAE25416 (1-1040)

QY 106 ATGGGGAGAGAGGCTGCTCAGCTCTCAGATGAGAGAAAGCAAGTCTCTCTC 165
DB 1 MetGlyGluGluGlySerAlaSerHisAspGluGluGluValLeu 20
QY 166 GAGCATCTCCGGGTGTGAATGCTCCAGAGAGCTTTTCAAGCAAGAGACCAAG 225
DB 21 GlyHisSerProGlyGluValCysSerGlnGluAlaGlnArgSerGln 40
QY 226 CTGCTCAGAGCTGCTGCTCTCAGAGGCTCCCTGGAAGCTTCAGAGTCTGAGTGGCTG 285
DB 41 LeuValGluLeuLeuValSerGlySerLeuGluGlyPheGluSerValLeuAspTyrLeu 60
QY 286 CTGCTCTGGAGAGTCTCTCTCTGGAGAGACTACAGAGGCTTCCACTCTGGAGCAAGCT 345
DB 61 LeuSerTyrPheValLeuSerTyrGluGlyPheHisLeuGlyGlnPro 80
QY 346 CTCTCCCACTGGCCAGGCGCTCTCTGGACACCGCTGGAATAGAGTAAGTGGGCTGT 405
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QY 406 CAGAAAGCTCATGCGGCTGCTCCAGAGAGCCAGAGCCAGAGCTCCCAAGCTGCAT 465
DB 101 GlnGlyLeuAlaAlaAlaGlnGluAlaGlnAlaAspSerGlnSerPheGlyHis 120
QY 466 GAGTCTGGAGAGCCCACTGCTCCAGAGAGCCAGAGCTGAGTCAAGGCGGAGCC 525
DB 121 GlyCysTyrAspPheHisSerLeuHisPheAlaArgAspLeuGlnSerHisArgProAla 140
QY 526 ATTGTCAAGAGCTTCAAGAGCCATGTTGAGAAATGCTGAGCCTGGCATGGAGGAGGT 585
DB 141 IleValArgArgLeuHisSerHisValGluAsnMetLeuAspLeuAlaTyrGly 160
QY 586 TTCCTCAGCCAGTATGAAATGATGAAATCAGAGTTCCTCAGACCGCTCCAGAGG 645
DB 161 PheValSerPheTyrGluCysAspLeuIleArgLeuProIlePheThrProSerGlnArg 180
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OM nucleic - protein search, using frame_plus_n2p model

Run on: January 7, 2004, 19:49:02 ; Search time 133.985 Seconds

(without alignments)
 13490.627 Million cell updates/sec

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Searched: 747907 segs, 201509753 residues

Total number of hits satisfying chosen parameters: 1495814

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 150 summaries

Command line parameters:

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Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	40	1209.5	14.6	953	9	US-09-728-721-8	Sequence 8, Appl
1	5448	65.9	1040	12	US-10-314-506-2	Sequence 2, Appl	41	1209.5	14.6	953	12	US-10-028-374-4	Sequence 4, Appl
2	5448	65.9	1040	14	US-10-014-269-2	Sequence 2, Appl	42	1209.5	14.6	953	12	US-10-028-374-4	Sequence 4, Appl
3	5448	65.9	1040	14	US-10-002-974-2	Sequence 2, Appl	43	1209.5	14.6	953	14	US-10-183-770-4	Sequence 8, Appl
4	5447	65.9	1040	14	US-10-002-974-67	Sequence 67, Appl	44	1209.5	14.6	953	14	US-10-183-770-4	Sequence 8, Appl
5	5445	65.8	1040	14	US-10-002-974-63	Sequence 63, Appl	45	1209.5	14.6	953	15	US-10-013-477-12	Sequence 12, Appl
6	5444	65.8	1040	14	US-10-002-974-69	Sequence 69, Appl	46	1209.5	14.6	953	15	US-10-013-477-12	Sequence 12, Appl
7	5443	65.8	1040	12	US-10-314-506-4	Sequence 4, Appl	47	1209.5	14.6	953	15	US-10-013-477-12	Sequence 12, Appl
8	5443	65.8	1040	14	US-10-014-269-4	Sequence 4, Appl	48	1209.5	14.6	953	15	US-10-013-477-12	Sequence 12, Appl
9	5443	65.8	1040	14	US-10-002-974-4	Sequence 4, Appl	49	1209.5	14.6	953	15	US-10-013-477-12	Sequence 12, Appl
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QY	166	GGACATCTCCGGGTGTGAATGTCTCCGAGAGGCTTTTCAGGACAGAGAGCGAG	225	Sequence 2, Appl
DB	21	GlyHisSerProGlyCysGluWetCysSerGlnGluAlaGlnArgSerGln	40	Sequence 170, App
QY	226	CTGGTCAAGCTGCTGCTTCAGAGGTCCTTGGAAGGCTTCGAGAGTCTGAGCTGGCTG	285	Sequence 8, Appl
DB	41	LeuValGluLeuLeuValSerGlySerLeuGluGluYpHeuLusSerValLeuAspTrpLeu	60	Sequence 16, Appl
QY	286	CTGTCTGGGAGGTCCTCTCTCTGGGAGAGCTACAGAGGCTTCAGAGGCTCGGAGCGCT	345	Sequence 16, Appl
DB	61	LeuSerTrpGluValLeuSerTrpGluAspTrpGluGluYpHeuLusLeuGluGlnPro	80	Sequence 43, Appl
QY	346	CTCTCCCACTGGCCAGGCGCTTCTGAGACAGCTCGAATTAAGGTAATTGGGCTGT	405	Sequence 70, Appl
DB	81	LeuSerHisLeuAlaArgArgLeuLeuAspTrpValTrpAsnLysGlyTrpTrpAlaCys	100	Sequence 13, Appl
QY	406	CGAAGCTCATCGGCGCTGCGCAAGAGGCTTCAGAGGCTTCAGAGGCTTCAGAGGCT	465	Sequence 2566, Ap

RESULT 1
 US-10-314-506-2
 / Sequence 2, Application US/10314506
 / Publication No. US20030175762N1
 / GENERAL INFORMATION:
 / APPLICANT: Nunez, Gabriel
 / APPLICANT: Inohara, Naohiro
 / APPLICANT: Ogura, Yasunori
 / TITLE OF INVENTION: Modulators of NOD2 signaling
 / FILE REFERENCE: UM-06984
 / CURRENT APPLICATION NUMBER: US/10/314,506
 / CURRENT FILING DATE: 2002-12-09
 / PRIOR APPLICATION NUMBER: US/10/314,269
 / PRIOR FILING DATE: 2001-10-26
 / PRIOR APPLICATION NUMBER: 60/244,299
 / PRIOR FILING DATE: 2000-10-30
 / NUMBER OF SEQ ID NOS: 62
 / SOFTWARE: PatentIn version 3.1
 / SEQ ID NO 2
 / LENGTH: 1040
 / TYPE: PRT
 / ORGANISM: Homo sapiens
 US-10-314-506-2

Alignment Scores:
 Pred. No.: 0
 Score: 5448.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 65.88%
 Gaps: 0

Db 101 GlnIysLeuIleAlaAlaLeGlnIuAlaGlnAlaAspSerGlnSerProIysLeuHis 120
QY 466 GGCTGCTGGACCCCCACTCGCTCCACCCAGCCGAGACTGCAAGCTCCAGCCGACCC 525
Db 121 GlyCysTrpAspProHisSerLeuHisProAlaArgSLeuGlnSerHisArgProAla 140
QY 526 ATGTGAGAGAGCTCCACAGCCATGTGGAGAAACATGCTGACCTGGCATGGAGAGGGAGT 585
Db 141 IleValAlaArgIleuHisSerHisValGluAsnMetLeuAspLeuAlaTrpGluArgGly 160
QY 586 TTGCTACGCCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 645
Db 161 PheValSerGlnTrpGluCysAspGluIleArgLeuProIlePheThrProSerGlnArg 180
QY 646 GCAAGAGGCTGCTGATCTTGCCACGGTGAAGCAAGCAAGTGGCTGCTGCTCTCA 705
Db 181 AlaArgArgLeuLeuAspLeuAlaThrValLysAlaAsnGlyLeuAlaAlaPheLeu 200
QY 706 CAACATGTTCCAGAAATTACCAAGTCCCATGGCCCTGCTTGGAGAGCTGCCATGGCAG 765
Db 201 GlnHisValGlnGlnIleuProValProLeuAlaLeuProLeuGluAlaAlaThrCysLys 220
QY 766 AAGTATATGGCCAAAGCTGAGAGCAAGGAGTGTCTGCTCAAGTCTGCTTCTCACTACT 825
Db 221 LysTrpMetAlaLysLeuArgThrThrValSerAlaGlnSerArgPheLeuSerThrTyr 240
QY 826 GATGAGCAGAGAGCGCTGCTGCTGAGAGCATATACAGAAATGCTCGAGAGTCTGG 885
Db 241 AspGlyAlaGlnThrLeuCysLeuGlnuAsp11eTyrThrGluAsnAlaLeuGluValTrp 260
QY 886 GCAAGTGTGGCATGGCTGGACCCCGCAGAAAGCCCAAGCCCGCTGGGCTGGAGAG 945
Db 261 AlaAspValGlyMetAlaGlyProProGlnLysSerProAlaThrLeuGlyLeuGlnu 280
QY 946 CTCTTCAGCAAGCCCTGGCCACTCAATGACATGCGGACATGCTGCTGGTGGGTAG 1005
Db 281 LeuPheSerThrProLysIleLeuAsnAspAlaAspThrValLeuValValGlyGln 300
QY 1006 GCGGCAGTGGCAAGACGCTCTGCAAGCGGCTGCATCTGCTGGGCTGGAGGCA 1065
Db 301 AlaGlySerGlyLysSerThrLeuLeuGlnArgLeuHisLeuLeuTrpAlaAlaGlyGln 320
QY 1066 GACTTCAGGAATTTCTCTTGTCTTCACATTCAGCTGGCCGAGCTGCGAGTGCATGGCC 1125
Db 321 AspPheGlnGlnuPheLeuPheValPheProPheSerCysArgGlnLeuGlnCysMetAla 340
QY 1126 AAACCACTCTGTGCGGACTTACTCTTTGAGGACTGCTGTTGGCTGATGTGTCAA 1185
Db 341 LysProLeuSerValArgThrLeuPheGlnuHisCysCysTrpProAspValGlyGln 360
QY 1186 GAAGACATCTTCAGTTACTCTCTGACCAAGCTGACCGTGTCTTAACTTTGATGGC 1245
Db 361 GluAspIlePheGlnLeuLeuAspHisProAspArgValLeuLeuThrPheAspGly 380
QY 1246 TTGACAGATTCAAGTTCAGGTTCAAGATGATGACGCGACTGCTCCCGACGACGCC 1305
Db 381 PheAspGluPheLysPheArgPheThrAspArgGluArgHisCysSerProThrAspPro 400

QY 1306 ACCTCTGTCAGAACCTGCTCTTCAACCTTCTGCAAGGCAACCTGCTGAAGATGCCGCC 1365
Db 401 ThrSerValGlnThrLeuLeuPheLeuLeuGlnGlyAsnLeuLeuLysAsnAlaArg 420
QY 1366 AAGGTGTGACAGCCCGTCCGCGCGCTGTGTGCGGCTCTCTCAGAGAAATGATCCGAC 1425
Db 421 LysValValThrSerArgProAlaAlaValSerAlaPheLeuArgLysTrpIleArgThr 440
QY 1426 GAATTCAACTCAAGGAGCTTCTCTGACAGAGGAGCATGAGTGTGACTGAGAGAGCGCAT 1485
Db 441 GluPheAsnLeuLysGlyPheSerGlnuGlnuLysIleGluLeuTrpLeuArgLysArgHis 460
QY 1486 CATTAGCCCCGGGTGGGAGACCGCTCATCCGCTGCTCCAAAGAACCTCAGCCCTGCAC 1545
Db 461 HisGluProGlyValAlaAspArgLeuIleArgLeuLeuGlnuGlnuThrSerAlaLeuHis 480
QY 1546 GATTGTGCAACCTGCTGCTCTCATGATGATGTGCAAAATGCCACCAAGAACTGTG 1605
Db 481 GlyLeuCysHisLeuProValPheSerTrpMetValSerLysCysHisGlnuLeuLeu 500
QY 1606 CTGCAAGAGGCGGAGGCTCCCAAGACACTACAGATATGTAAGTCTGCTGATTTGCAAG 1665
Db 501 LeuGlnuGlnuLysLysSerProLysThrThrAspMetCysLeuLeuIleLeuGlnHis 520
QY 1666 TTTCTGCTGATGCCACCCCGCCAGACTCAGCTGCCAAGGCTGGACCCGACTCTCT 1725
Db 521 PheLeuLeuHisAlaThrProProAspSerAlaSerGlnuLysLeuLysProSerLeuLeu 540
QY 1726 CCGGCGCGGCTCCCAACCTCTGCAACCTGGGCAAGTGGCTGTGGGAGGCTGGGCAAG 1785
Db 541 ArgGlyArgLeuProThrLeuLeuHisLeuGlyArgLeuAlaLeuTrpGlyLeuGlyMet 560
QY 1786 TGTGCTAAGTGTCTCAAGCCAGAGCTCCAGAGCAAGTCAAGCTGATGATCACT 1845
Db 561 CysCysTrpValPheSerAlaGlnuGlnuAlaAlaGlnValSerProAspAspIle 580
QY 1846 TCTCTTGGCTTCTGTGTGCTGCAAGAGTGTGCTGCCAGGAGTACGAGCGCCCTGGAA 1905
Db 581 SerLeuGlyPheLeuValArgAlaLysGlyValValAlaProGlySerThrAlaProLeuGln 600
QY 1906 TTCTTCAACTCACTTTCCAGTGTCTTCTGCGCGGCTTCACTGGCACTCAAGTGTGAT 1965
Db 601 PheLeuHisIleThrPheGlnCysPheSerAlaAlaPheTyrLeuAlaLeuSerAlaAsp 620
QY 1966 GTGCCACCACTTTGCTCAGACACCTCTCAATGTGGCAGGCAAGGCACTCAACCATG 2025
Db 621 ValProProAlaLeuLeuArgHisLeuPheAsnCysGlyArgProGlyAsnSerProPhe 640
QY 2026 GCCAGGCTCTGCCCAAGATGTGCAATCCAGGCTCGAGAGGAAAGACAGACCGTGGCA 2085
Db 641 AlaArgLeuLeuProThrMetCysIleGlnAlaSerGlnuLysLysAspSerValAla 660
QY 2086 GCTTGTGTCAGAGAGCGCGCAAGCAACTTCAAGTCAAGCAAGCTTCTGCGGAGG 2145
Db 661 AlaLeuLeuHisLysAlaGluProHisAsnLeuGlnIleThrAlaAlaPheLeuAlaGly 680

QY 2146 CTGTGTCCCGGAGCACTGGGGCCTGTGTGCTGAGTGCACACATCTGAGAGAGCCCTG 2205
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 Db 681 LeuLeuSerPArgLuhHstRpgLylLeuLeuAlaGluCysGlnHnSerGluLysAlaLeu 700
 QY 2206 CTCGGCGCGCAGAGCCTGTGCCCGCTGGTGTCTGGCCCGCAGCCTCCGACAGCACTTCAC 2265
 |||||
 Db 701 LeuArgRgLnAlaCysAlaArgTrpCysLeuAlaArgSerLeuAlaGlySHisPheHis 720
 QY 2266 TCATATCCCGCAGCTGCACCGGGGTAGGCCAGAGCCTGCATGCCATGCCCGGGTTATC 2325
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 Db 721 SerLeProProlaAlaProGlyAlaLysSerValHisAlaMetProGlyPheHis 740
 QY 2326 TGGCTCATCCGAGAGCCTGTACAGATGCAGAGAGAGCGGCTGGCTCGAAGAGCTCACT 2385
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 Db 741 TrpLeuLlaArgSerLeuTrgluMetGlnGluGluArgLeuAlaArgLysAlaAlaArg 760
 QY 2386 GGCTGAAATGCTGGGACACTCAAGTATGACATTTTGCAGTGTGGGCCCACTGAGTGTCT 2445
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 Db 761 GlyLeuAsnValGlyHisLeuLysLeuThrPheCysSerValGlyProThrGluCysAla 780
 QY 2446 GCCCTGGCCTTGTGTGTCAGACCTCCGCGGGCCCTGGCCCTGCACTGGAGCTACAC 2505
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 Db 781 AlaLeuAlaPheValLeuGlnHnIleuAlaArgAlaProValAlaLeuGlnLeuAspTrpAsn 800
 QY 2506 TCTGTGGGTGACATTTGGCTGGAGGACCTGTGCTTGCCTTGGTGTGTGCAAGGCTCTG 2565
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 Db 801 SerValGlyAspLLeGlyValGlnGlnLeuProCysLeuGlyValCysLysAlaLeu 820
 QY 2566 TATTGGCGCAATTAACATATCTCAGACCGAGGCATCTGCAGCTCATTAATGTGCTT 2625
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 Db 821 TyrLeuArgPAspAsnHnIleSerPAspArgGlyLleCysLysLeuLleGluCysAlaLeu 840
 QY 2626 CACTGCAGCAATTCAGAAATTAGCTTATTCACACAAATTGACTGACGCTGTGCA 2685
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 Db 841 HisCysGluGlnLeuGlnLysLeuAlaLeuPheAsnLysLeuThrAspGlyCysAla 860
 QY 2686 CACTGCATGGCTAAGCTCCTTGCATGCAGGCAAACTTCTTGGCATTAAGGCTGGGAA 2745
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 Db 861 HisSerPheAlaLysLeuLeuAlaCysArgGlnAsnPheLeuAlaLeuArgLeuGlyAsn 880
 QY 2746 AACTACATCACTGCCGCGGGAACCAAGTGTGGCTGGCGAGGGGCTCCGAGGCAACACTCC 2805
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 Db 881 AsnTyrLleThrAlaAlaGlyAlaGlnValLeuAlaGluGlyLeuArgGlyAsnThrSer 900
 QY 2806 TTGCAGTCTCTGGGATTTCTGGGGCAACAAGTGGGTACAGAGGGGCCCAAGCCTGGCT 2865
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 Db 901 LeuGlnPheLeuGlyPheTrpGlyAsnArgValGlyAspGluGlyAlaGlnAlaLeuAla 920
 QY 2866 GAAAGCTTGGGTGATCACAGAGCTTGAAGTGGCTGAGCTGTGTGGGGAACAACATTGGC 2925
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 Db 921 GluAlaLeuGlyAspHisGlnSerLeuArgTrpLeuSerLeuValGlyAsnAsnLleGly 940
 QY 2926 AGTGTGGGTGCCCAAGCTTGGCACTGATGCTGGCAAAAGACGTCATGCTAGAGAACTC 2985
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 Db 941 SerValGlyAlaGlnAlaLeuAlaLeuMetLeuAlaLysAsnValIleThrLeuGluGlnLeu 960
 QY 2986 TGGCTGGAAGAGAAACATCTCCAGATGAAAGGTGTATGTTCTCTCCGACAGAGCACTGAAG 3045

Db 961 CysLeuGluGlnLysHnHisLeuGlnAspGluGlyValCysSerLeuAlaGluGlyLeuLys 980
 QY 3046 AAAAATTCAAGTTTGAATAATCTGAAGTGTCCATTAAGTGCATCACTACCTACCTAGGGGGA 3105
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 Db 981 LysAsnSerSerLeuLysLleLeuLysLeuSerPAsnAsnCysLleThrTyrLeuGlyAla 1000
 QY 3106 GAAAGCCTTCTGCAAGGCCCTTGAAGAAGATGACACATCTCTGAAAGTCTGGCTCCGAGG 3165
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 Db 1001 GluAlaLeuLeuGlnAlaLeuGluArgAsnAspThrLleLeuGluValTrpLeuArgGly 1020
 QY 3166 AACACTTCTCTTACAGAGAGGTGACAAAGCTGGGCTGCAGGGAACACAGACTGTGCTT 3225
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 Db 1021 AsnThrPheSerLeuGluGlnLysValAspLysLeuGlyCysArgPAspThrArgLeuLeu 1040

Search completed: January 7, 2004, 20:49:14
 Job time : 432.985 secs

OM nucleic - protein search, using frame_plus_n2p model

Run on: January 7, 2004, 19:24:11 ; Search time 65.4927 Seconds

(without alignments)
13171.439 Million cell updates/sec

Title: US-10-014-269-1
Perfect score: 8270
Sequence: 1 gtagacagatccagctccac.....atgaacgttgatcaaac 4485

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283308 seqs, 96166682 residues
Total number of hits satisfying chosen parameters: 566616

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Command line parameters:
-MODE=frame_plus_n2p.model -DEV=xlp

Q=/cgn2_1/USPTO_spool_p/US10014269/rnat_07012004_175229_24535/app_query.fasta_1
-9358
-DB=PIR_76 -QMT=fastan -SUFFIX=fpr -MINMATCH=0.1 -LOOFCI=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=150
-DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=50 -MODE=LOCAL
-OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=us10014269@cgn_1_1_224@rnat_07012004_175229_24535 -NCPU=6 -ICPU=3
-NO_MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPLICOR=100 -LONGLIG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
-Fgapext=7 -Ygapop=10 -Ygapext=0.5 -Delop=6 -Delext=7

Database : PIR_76**
1: pir1**
2: pir2**
3: pir3**
4: pir4**

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

		Result		Query		DB	ID	Description
No.	Score	Match	Length	DB	ID			
1	433	5.2	1130	2	A48843			MHC class II trans
2	393.5	4.8	1192	2	T17255			hypothetical prote
3	365.5	4.4	1111	2	A59000			matern protein (imp
4	337	4.1	1466	1	CGH07L			collagen alpha 1(I
5	320	3.9	1453	2	S21626			collagen alpha 1(I
6	314.5	3.8	1373	1	A43281			collagen alpha 1(I
7	314.5	3.8	1464	2	S59856			collagen alpha 1(I
8	312.5	3.8	1464	2	S59856			collagen alpha 1(I
9	312	3.8	784	2	U03037			hypothetical 82K P
10	311	3.8	1464	2	CGH07S			collagen alpha 1(I
11	308.5	3.8	1660	1	Q0BE3			BHLFI protein - hu
12	308	3.8	2944	2	A54849			collagen alpha 1(I
13	303	3.7	1466	1	CGH07L			collagen alpha 1(I
14	301.5	3.6	1691	1	S22917			collagen alpha 5(I
15	301	3.7	1496	1	CGH07V			collagen alpha 2(I
16	300.5	3.7	1049	1	CGH07S			collagen alpha 1(I
17	294.5	3.6	1049	1	CGH07S			collagen alpha 1(I
18	294	3.6	779	1	CGH07S			collagen alpha 1(I
19	292.5	3.6	1414	1	S23809			collagen alpha 2(I
20	291.5	3.5	1487	1	CGH06C			collagen alpha 2(I
21	290	3.5	1690	1	CGH07L			collagen alpha 1(I
22	289	3.5	886	2	I50694			collagen alpha 4(I
23	287.5	3.5	1366	1	CGH02S			collagen alpha 2(I
24	287.5	3.5	1670	1	CGH03B			collagen alpha 3(I
25	287	3.5	886	2	I50694			collagen alpha 1(I
26	286.5	3.5	1418	2	T45467			collagen alpha 1(I
27	286.5	3.5	2715	2	T13049			eyelid - fruit fly
28	284	3.5	671	1	CGH07S			collagen alpha 1(I
29	282	3.4	2944	2	A54849			collagen alpha 1(I
30	281.5	3.4	1806	1	CGH07E			collagen alpha 1(I
31	281	3.4	1690	1	CGH07B			collagen alpha 4(I
32	280.5	3.4	1414	1	S23809			collagen alpha 2(I
33	279.5	3.4	1466	1	CGH07E			collagen alpha 2(I
34	276	3.3	1453	2	S21626			collagen alpha 1(I
35	275	3.3	1042	1	CGH07S			collagen alpha 1(I
36	274	3.3	1497	2	T45467			collagen alpha 1(I
37	271.5	3.3	1418	2	T45467			collagen alpha 1(I
38	271.5	3.3	1419	2	A41182			collagen alpha 1(I
39	271.5	3.3	1487	2	B41182			collagen alpha 1(I
40	271	3.3	456	2	A31857			ribonuclease inhib
41	270	3.3	1419	2	A41182			collagen alpha 1(I
42	270	3.3	1487	2	B41182			collagen alpha 1(I
43	264.5	3.2	1838	1	CGH07V			collagen alpha 1(I
44	264	3.2	1585	2	T31611			hypothetical prote
45	263.5	3.2	1496	1	CGH07V			collagen alpha 2(I
46	263	3.2	1487	1	CGH06C			collagen alpha 1(I
47	263	3.2	1669	1	CGH54B			collagen alpha 1(I
48	262.5	3.2	1464	1	CGH07S			collagen alpha 1(I
49	262	3.2	1042	1	CGH07S			collagen alpha 1(I
50	258.5	3.1	1492	2	A40333			collagen alpha 1(I
51	258.5	3.1	1763	2	S16366			collagen alpha 1(I
52	258.5	3.1	1806	1	CGH07E			collagen alpha 1(I
53	258.5	3.1	1843	2	S18803			collagen alpha 1(I

54	258	3.1	1492	2	A4033	collagen alpha 1(V
55	257	3.1	1779	2	CG6015	collagen alpha 1(V
56	257	3.1	1843	2	S15803	collagen alpha 1(V
57	256.5	3.1	1669	1	CGH048	collagen alpha 1(V
58	256.5	3.1	1838	1	CGH01V	collagen alpha 1(V
59	255.5	3.1	888	2	S28791	collagen alpha 1(X
60	255.5	3.1	1691	1	S22917	collagen alpha 5(I
61	252.5	3.1	2715	2	T13049	eyelid - fruit fly
62	252	3.0	660	1	Q08E3	BHLF protein - hu
63	252	3.1	1603	2	S23810	collagen alpha 1(X
64	251.5	3.0	1486	1	B40333	collagen alpha 1(I
65	250.5	3.1	1486	1	B40333	collagen alpha 1(I
66	250	3.0	1373	1	A43291	collagen alpha 2(I
67	248.5	3.0	1603	2	S23810	collagen alpha 1(X
68	247.5	3.0	1670	1	CGH03B	collagen alpha 3(I
69	246.5	3.0	920	2	B34433	collagen alpha 1(I
70	244.5	3.0	1366	1	CGH02S	collagen alpha 2(I
71	243	2.9	1357	2	T2365	hypothetical prote
72	242	2.9	4957	2	T03455	ALR protein - huma
73	242	2.9	5262	2	T03455	collagen alpha 1(V
74	241	2.9	744	1	A34246	collagen alpha 1(V
75	241	2.9	744	1	S23238	collagen alpha 1(V
76	240.5	2.9	964	1	CGH02S	collagen alpha 2(I
77	240.5	2.9	1497	2	T48607	collagen alpha 2(I
78	240.5	2.9	1346	1	CGH02E	collagen alpha 2(X
79	239.5	2.9	920	2	A45748	collagen alpha 1(V
80	239.5	2.9	1549	2	T48103	type VII collagen
81	239	2.9	1460	1	EDBE1F	immediate-early pr
82	238.5	2.9	627	2	A44112	spidrin 2, dragli
83	238.5	2.9	1549	2	T48103	type VII collagen
84	238	2.9	1428	2	T08652	lustrin A - Gallo
85	238	2.9	1738	2	T23350	hypothetical prote
86	238	2.9	1759	2	T23351	collagen alpha 2(I
87	238	2.9	1791	2	T02345	hypothetical prote
88	237.5	2.9	461	2	A31858	ribonuclease-angio
89	237.5	2.9	1344	1	A3175	mucin 1 precursor,
90	237.5	2.9	13288	2	T03099	mucin, submaxillar
91	237	2.9	1446	1	A43344	immediate-early pr
92	236.5	2.9	1763	2	S16366	collagen alpha 2(I
93	235.5	2.9	1106	2	J00405	hypothetical 119.5
94	235.5	2.9	1106	2	J00405	hypothetical 119.5
95	235.5	2.9	1759	2	T23351	collagen alpha 2(I
96	235	2.8	1712	1	CGH02B	collagen alpha 1(I
97	234.5	2.8	931	2	S13580	collagen alpha 1(I
98	234.5	2.9	1758	2	T23350	hypothetical prote
99	234	2.8	1691	1	CGH06B	collagen alpha 6(I
100	233.5	2.8	1691	1	CGH06B	collagen alpha 6(I
101	232	2.8	456	2	S20597	ribonuclease inhib
102	231.5	2.8	1707	2	A33526	collagen alpha 2(I
103	231	2.8	754	2	A55267	collagen alpha 5(I
104	231	2.8	920	2	A45748	collagen alpha 1(V
105	229.5	2.8	1585	2	T31611	hypothetical prote
106	229.5	2.8	3198	2	A44246	collagen alpha 2 F
107	228	2.8	825	2	JC4163	DNA-binding protei
108	228	2.8	1774	2	B56101	collagen alpha 1(X
109	226.5	2.7	1532	2	A61262	collagen alpha 1(X
110	226.5	2.7	1707	2	A33526	collagen alpha 2(I

111	226	2.7	1315	2	A56101	collagen alpha 1(X
112	226	2.7	1360	2	T33922	hypothetical prote
113	225	2.7	1024	2	S18251	collagen alpha 1(X
114	223.5	2.7	1027	2	S28774	collagen alpha cha
115	223	2.7	1024	2	S18251	collagen alpha 1(X
116	222.5	2.7	1446	1	A45344	immediate-early pr
117	222	2.7	671	1	CGRT1S	collagen alpha 1(I
118	222	2.7	1574	2	T13954	MEGF6 protein - ra
119	222	2.7	1752	2	A43407	collagen alpha 3(I
120	221.5	2.7	535	2	T48102	RAN GTPase activat
121	221.5	2.7	964	1	CGH02B	collagen alpha 2(I
122	221.5	2.7	2142	2	B35098	MHC class III hist
123	221	2.7	506	2	A45841	T-complex-associat
124	221	2.7	789	2	T52067	hypothetical prote
125	218.5	2.6	2232	2	T14434	hypothetical prote
126	218	2.6	677	2	S23286	collagen alpha 1(V
127	218	2.6	744	2	S13435	collagen alpha 1(V
128	218	2.7	1712	1	CGH02B	collagen alpha 2(I
129	217	2.6	533	2	T52063	ran GTPase-activat
130	217	2.6	1870	2	S37671	MHC class III hist
131	216.5	2.6	1872	2	S36152	MHC class III hist
132	216.5	2.6	2321	2	S78549	notch3 protein - h
133	215.5	2.6	743	1	S23779	collagen alpha 1(V
134	215.5	2.6	921	2	S42617	collagen alpha 1(I
135	215	2.6	635	2	A57131	collagen alpha 2(V
136	214.5	2.6	635	2	A57131	collagen alpha 2(V
137	214.5	2.6	1344	1	A55175	collagen alpha 2(V
138	214	2.6	1184	2	S50832	mucin 1 precursor,
139	213.5	2.6	920	2	B34493	collagen alpha 1(I
140	213.5	2.6	931	2	S13580	collagen alpha 1(I
141	213	2.6	1075	2	T31668	hypothetical prote
142	213	2.6	1460	1	EDBE1F	immediate-early pr
143	212.5	2.6	631	2	C89243	protein F28C1.3 (I
144	212.5	2.6	631	2	T21471	hypothetical prote
145	212.5	2.6	1574	2	T13954	MEGF6 protein - ra
146	212.5	2.6	2796	2	JC4743	fatly-acid synthas
147	212	2.6	825	1	EDBE1D	immediate-early pr
148	211.3	2.6	1964	2	T09059	notch4 - mouse
149	211	2.6	730	2	A36226	collagen alpha 1 c
150	211	2.6	3570	2	T45025	mucin MUC5B, trach

Search completed: January 7, 2004, 19:47:12
Job time : 478.493 secs

OM nucleic - protein search, using frame_plus_n2p model

Run on: January 7, 2004, 19:24:01 ; Search time 34,7461 Seconds
(without alignments)
12140.333 Million cell updates/sec

Title: US-10-014-269-1
Perfect score: 8270
Sequence: 1 gtagacagacccagcgcac.....ataactgtgagtcacaaac 4485

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 127863 seqs, 47026705 residues
Total number of hits satisfying chosen parameters: 255726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Command line parameters:

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-Q=/cgn2_1/USPTO_spool_p/US10014269/runat_07012004_175229_24504/app_query.fasta_1
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-DB=SwissProt_41 -OFMT=fastan -SUFFIX=exp -MINMATCH=0.1 -LOOPECL=0 -LOOPEXT=0
-DBITS-bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdf -LIST=150
-DOCALLIGN=200 -THR_SCORE=perc -THR_MAX=100 -THR_MIN=0 -ALIGN=90 -MODE=LOCAL
-OUTFMT=ptc -NORW=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10014269 -GCEN_1_1_97 -runat_07012004_175229_24504 -NCPU=6 -ICPU=3
-NO_MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
-Fgapext=7 -Ygapop=10 -Ygapext=0.5 -Delop=6 -Delext=7

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result Query
No. Score Match Length DB ID Description

1	5448	65.9	1040	1	CARF_HUMAN	Q9hcz9	homo sapien
2	4196	50.7	1020	1	CARF_MOUSE	Q9K320	mus musculus
3	1222.5	14.8	953	1	CAR4_MOUSE	Q8bhd0	mus musculus
4	1209.5	14.6	953	1	CAR4_HUMAN	Q9Y239	homo sapien
5	532.5	6.4	1062	1	PYA7_HUMAN	P59046	homo sapien
6	505.5	6.1	1033	1	CIS1_MOUSE	Q8r4b8	homo sapien
7	497	6.0	1034	1	CIS1_HUMAN	Q96p20	homo sapien
8	433	5.2	1130	1	C27A_HUMAN	P33076	homo sapien
9	425	5.1	1155	1	C27A_MOUSE	P79621	mus musculus
10	410.5	5.0	1473	1	NAL4_HUMAN	Q9c000	homo sapien
11	396	4.8	994	1	NAL4_MOUSE	Q96mz2	homo sapien
12	385.5	4.7	854	1	PYA5_RAT	Q63035	rattus norvegicus
13	385	4.7	980	1	PYA3_HUMAN	Q8w902	homo sapien
14	379.5	4.6	1062	1	NAL2_HUMAN	Q8w902	homo sapien
15	366	4.4	892	1	PYA5_HUMAN	P59044	homo sapien
16	365.5	4.4	1111	1	PYA5_MOUSE	Q9ctms	mus musculus
17	360.5	4.4	843	1	PYA5_MOUSE	Q91ws2	mus musculus
18	355.5	4.3	1200	1	CAL3_HUMAN	P59047	homo sapien
19	337	4.1	1466	1	CAL3_MOUSE	P02461	homo sapien
20	322	3.9	1464	1	CAL3_MOUSE	P08121	mus musculus
21	320	3.9	1453	1	CAL1_MOUSE	P11087	mus musculus
22	314.5	3.8	1372	1	CAL1_MOUSE	Q01149	mus musculus
23	313	3.8	1464	1	CAL1_HUMAN	P02452	homo sapien
24	312	3.8	1764	1	YAV2_HUMAN	P14728	xenopus laevis
25	310	3.7	1033	1	PYA6_HUMAN	P59045	homo sapien
26	308.5	3.8	660	1	YHLL_EBV	P03181	epstein-barr virus
27	308	3.7	2944	1	CAL7_HUMAN	Q02388	homo sapien
28	307.5	3.7	1464	1	CAL3_MOUSE	P08121	mus musculus
29	305	3.7	1460	1	CAL1_MOUSE	Q9Kxj7	canis familiaris
30	303	3.7	1466	1	CAL3_HUMAN	P02461	homo sapien
31	301	3.7	1496	1	CAL3_HUMAN	P03997	homo sapien
32	297.5	3.7	1049	1	CAL3_BOVIN	P04258	bos taurus
33	297.5	3.6	1685	1	CAL3_HUMAN	P29400	homo sapien
34	294.5	3.6	1049	1	CAL3_BOVIN	P04258	bos taurus
35	294	3.6	779	1	CAL1_BOVIN	P02453	bos taurus
36	291.5	3.5	1418	1	CAL2_HUMAN	P02458	homo sapien
37	290.5	3.5	1262	1	CAL3_CHICK	P08123	homo sapien
38	290	3.5	1690	1	CAL4_HUMAN	P12105	gallus gallus
39	289.5	3.5	1364	1	CAL2_HUMAN	P53420	homo sapien
40	288.5	3.5	1364	1	CAL2_BOVIN	P02465	bos taurus
41	287	3.5	1262	1	CAL3_CHICK	P12105	gallus gallus
42	284.5	3.5	1372	1	CAL2_RAT	P02466	rattus norvegicus
43	282.5	3.4	1670	1	CAL3_HUMAN	Q01955	homo sapien
44	282	3.4	2944	1	CAL1_HUMAN	Q02388	homo sapien
45	281	3.4	671	1	CAL1_RAT	P02453	rattus norvegicus
46	281	3.4	1690	1	CAL4_HUMAN	P53420	homo sapien
47	279	3.4	1736	1	CAL2_HUMAN	P13942	homo sapien
48	276	3.4	1453	1	CAL1_CHICK	P02457	gallus gallus
49	276	3.3	1453	1	CAL1_MOUSE	P11087	mus musculus
50	275.5	3.4	1459	1	CAL2_MOUSE	P26481	mus musculus
51	273	3.3	1460	1	CAL1_MOUSE	Q9Kxj7	canis familiaris
52	271	3.3	486	1	RINI_PIG	P10775	sus scrofa
53	270	3.3	1459	1	CAL2_MOUSE	P26481	mus musculus
54	268.5	3.3	1806	1	CAL2_HUMAN	P12107	homo sapien
55	267	3.3	1395	1	CAL2_RANCA	Q42350	rana catesbeiana
56	266.5	3.2	1736	1	CAL2_HUMAN	Q64733	homo sapien
57	266	3.2	1464	1	CAL1_HUMAN	P02452	homo sapien

58	263.5	3.2	1496	1	CA25_HUMAN	P05997 homo sapien
59	263	3.2	1418	1	CA12_HUMAN	P02456 homo sapien
60	263	3.2	1669	1	CA14_MOUSE	P02463 mus musculu
61	262	3.2	1453	1	CA11_CHICK	P02457 gallus gall
62	258.5	3.1	1366	1	CA21_CANFA	P06392 canis famli
63	258.5	3.1	1763	1	CA24_ASCSU	P07393 ascaris suu
64	258.5	3.1	1838	1	CA15_HUMAN	P09098 homo sapien
65	257.5	3.1	1372	1	CA21_RAT	P02466 rattus norv
66	257	3.1	1779	1	CA11_BOVIN	P02453 bos taurus
67	256.5	3.1	1669	1	CA14_HUMAN	P02462 homo sapien
68	254.5	3.1	1366	1	CA21_CANFA	P06392 canis famli
69	254.5	3.1	1838	1	CA15_HUMAN	P09098 homo sapien
70	253	3.1	1362	1	CA21_CHICK	P02467 gallus gall
71	252	3.0	660	1	YHL1_EBV	P03181 Epstein-bar
72	252	3.1	1603	1	CA1F_HUMAN	P02092 homo sapien
73	251.5	3.0	1364	1	CA21_BOVIN	P02465 bos taurus
74	251.5	3.1	1670	1	CA14_HUMAN	P02462 homo sapien
75	251.5	3.1	1685	1	CA15_HUMAN	P09098 homo sapien
76	250.5	3.0	1804	1	CA1B_MOUSE	P29400 homo sapien
77	250	3.0	747	1	CA12_MOUSE	P02459 bos taurus
78	250	3.0	1372	1	CA21_MOUSE	P08123 homo sapien
79	249.5	3.0	1366	1	CA1F_HUMAN	P02092 homo sapien
80	248.5	3.0	1603	1	CA1F_HUMAN	P02092 homo sapien
81	248	3.0	1806	1	CA1B_HUMAN	P21207 homo sapien
82	247	3.0	1362	1	CA21_CHICK	P02467 gallus gall
83	245.5	3.0	1516	1	CA1H_HUMAN	P09060 homo sapien
84	244	3.0	2003	1	NTC4_HUMAN	P09466 homo sapien
85	243.5	3.0	747	1	CA12_BOVIN	P02467 gallus gall
86	241.5	2.9	1356	1	CA21_ONCMY	P02459 bos taurus
87	241	2.9	744	1	CA1B_RABIT	P03484 oncomyocnu
88	240.5	2.9	1804	1	CA1B_MOUSE	P12422 oryctolagus
89	239	2.9	1736	1	CA2B_HUMAN	P02463 mus musculu
90	238.5	2.9	627	1	SPD2_NEPCL	P13942 homo sapien
91	238.5	2.9	1255	1	MUC1_HUMAN	P46804 nephila cla
92	238	2.9	1758	1	CA24_CAEEL	P15341 h mucin 1 p
93	237.5	2.9	460	1	RINI_HUMAN	P17140 caenorhabd
94	237	2.9	1446	1	IE1B_PPRXA	P13489 homo sapien
95	236.5	2.9	921	1	CA19_HUMAN	P03479 pseudorab
96	236.5	2.9	1763	1	CA24_ASCSU	P20849 homo sapien
97	236	2.9	1355	1	CA21_RANCA	P27393 ascaris suu
98	235.5	2.8	1024	1	CARQ_HUMAN	O42350 rana cateab
99	235	2.8	1712	1	CA24_HUMAN	P08572 homo sapien
100	234.5	2.9	1756	1	CA24_CAEEL	P17140 caenorhabd
101	233.5	2.8	815	1	PYGQ_DROME	P03498 drosophila
102	233.5	2.8	1669	1	CA14_MOUSE	P02463 mus musculu
103	232	2.8	466	1	RINI_RAT	P03415 rattus norv
104	232	2.8	1691	1	CA64_HUMAN	P08122 mus musculu
105	231.5	2.8	1707	1	CA54_MOUSE	P08247 canis famli
106	231	2.8	754	1	CA54_CANFA	P09646 homo sapien
107	230	2.8	1003	1	MBD6_HUMAN	O911b6 mus musculu
108	229	2.8	1403	1	B1RF_MOUSE	O94739 mus musculu
109	229.5	2.8	1736	1	CA2B_MOUSE	O911b6 mus musculu
110	229	2.8	1527	1	CA1H_MOUSE	O93061 mus musculu
111	228	2.8	823	1	5B5_RAT	O63003 rattus norv
112	226.5	2.7	1356	1	CA21_ONCMY	O93484 oncomyocnu
113	226.5	2.7	1707	1	CA24_MOUSE	P08122 mus musculu
114	225.5	2.7	1027	1	CAFE_RIFPA	P07054 riftia pach

c 115	225	2.7	911	1	CA1B_BOVIN	Q28083 bos taurus
c 116	222.5	2.7	1446	1	IE1B_PPRXA	P03479 pseudorab
c 117	222	2.7	671	1	CA11_RAT	P02454 rattus norv
c 118	221.5	2.7	1516	1	CA1H_HUMAN	P39060 homo sapien
c 119	221.5	2.7	1442	1	BAT2_HUMAN	P48634 homo sapien
c 120	220.5	2.7	1461	1	IE1B_PPRVF	P11675 pseudorab
c 121	219.5	2.7	743	1	CA1B_MOUSE	O0780 mus musculu
c 122	219.5	2.7	744	1	CA1B_HUMAN	P27658 mus musculu
c 123	218.5	2.6	911	1	CA1B_BOVIN	Q28083 bos taurus
c 124	218.5	2.6	2161	1	SHK1_HUMAN	O91666 homo sapien
c 125	218.5	2.7	2161	1	SHK1_HUMAN	O91666 homo sapien
c 126	218	2.6	1402	1	B1RG_MOUSE	O911b3 mus musculu
c 127	218	2.7	1712	1	CA24_HUMAN	P08572 homo sapien
c 128	218	2.6	1758	1	CA14_CAEEL	P17135 caenorhabd
c 129	216.5	2.6	867	1	SSPO_BOVIN	P98167 bos taurus
c 130	216.5	2.6	2321	1	NTC3_HUMAN	Q9um47 homo sapien
c 131	215	2.6	635	1	CA28_HUMAN	P25067 homo sapien
c 132	215	2.6	689	1	CA29_HUMAN	Q14055 homo sapien
c 133	214.5	2.6	635	1	IR52_HUMAN	P25067 homo sapien
c 134	214.5	2.6	1324	1	IR52_HUMAN	Q94742 homo sapien
c 135	213.5	2.6	921	1	CA19_HUMAN	P20849 homo sapien
c 136	213	2.6	1336	1	W146_HUMAN	O9c0j8 homo sapien
c 137	212.3	2.6	2167	1	SHK1_RAT	O9wv48 rattus norv
c 138	212	2.6	825	1	ICPQ_HSVZH	P28284 herpes slmp
c 139	212	2.6	1255	1	MUC1_HUMAN	P15941 h mucin 1 p
c 140	211.5	2.6	1403	1	B1RA_MOUSE	O9cwk5 mus musculu
c 141	211	2.6	5703	1	MUSE_HUMAN	Q14050 homo sapien
c 142	210	2.6	684	1	CA39_HUMAN	P02462 homo sapien
c 143	210	2.6	1669	1	CA14_HUMAN	Q14050 homo sapien
c 144	208.5	2.5	684	1	CA39_HUMAN	Q05722 mus musculu
c 145	208.5	2.5	921	1	CA1B_MOUSE	P31695 mus musculu
c 146	208	2.5	1964	1	NTC4_HUMAN	Q03692 homo sapien
c 147	208	2.5	1964	1	NTC4_MOUSE	P31695 mus musculu
c 148	208	2.5	3718	1	LM45_MOUSE	Q61001 mus musculu
c 149	207.5	2.5	1691	1	CA64_HUMAN	Q14031 homo sapien
c 150	206.5	2.5	1902	1	SWF1_HUMAN	O14497 homo sapien

ALIGNMENTS

RESULT 1						
CAFE_HUMAN						
ID	CAFE_HUMAN	STANDARD	PRT	1040	AA.	
AC	Q9RHCZ; Q96RH5; Q96RH6; Q96RH9;					
DT	28-FEB-2003 (Rel. 41, Created)					
DR	28-FEB-2003 (Rel. 41, Last sequence update)					
DT	15-SEP-2003 (Rel. 42, Last annotation update)					
DE	Caspase recruitment domain protein 15 (Nod2 protein) (Inflammatory					
DE	bowel disease protein 1).					
OS	CAERD15 OR NOD2 OR IBD1.					
OS	Homo sapiens (Human).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.					
OX	NCBI_Taxid=9606;					
RY	[1]					
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), MUTAGENESIS OF LYS-305, AND					
RP	VARIANT ARG-908.					

CC TISSUE=Breast;
 RX PubMed=1087742;
 RA Ogura Y., Inohara N., Benito A., Chen F.F., Yamaoka S., Nunez G.;
 RT "Nod2, a Nod1/Apar-1 family member that is restricted to monocytes and
 RL J. Biol. Chem. 276:4812-4818(2001).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), VARIANTS CD THR-140; ARG-157;
 RP CYS-235; ARG-248; SER-268; SER-289; ASN-291; VAL-301; TRP-311;
 RP VAL-348; ARG-352; CYS-373; SER-414; LEU-431; VAL-432; LYS-441;
 RP VAL-612; THR-612; TRP-664; TRP-702; CYS-703; CYS-713; GLY-723;
 RP VAL-753; VAL-758; LYS-778; MET-793; LYS-843; SER-853; VAL-863;
 RP ARG-908; ASP-918; ASP-924 AND ILE-955, VARIANTS ULCERATIVE COLITIS
 RP THR-140 AND THR-885, AND VARIANT MET-189.
 RC TISSUE=Leukocyte;
 RX MEDLINE=21279172; PubMed=11385576;
 RA Hugot J.-P., Chamaillard M., Zouali H., Lesage S., Cezaud J.-P.,
 RA Belaiche J., Almer S., Tyek C., O'Morain C.A., Gassull M., Binder V.,
 RA Finkel Y., Cortot A., Modigliani R., Laurent-Puig P.,
 RA Gower-Rousseau C., Macry J., Colombel J.-F., Sabaathou M., Thomas G.;
 RT "Association of NOD2 leucine-rich repeat variants with susceptibility
 RT to Crohn's disease.";
 RL Nature 411:599-603(2001).
 RN [3]
 RP VARIANTS BS GLN-334; TRP-334 AND PHE-469.
 RX MEDLINE=21418644; PubMed=11528384;
 RA McCelli-Richard C., Lesage S., Rybojard M., Prieur A.M.,
 RA Manouvrier-Hanu S., Hafner R., Chamaillard M., Zouali H., Thomas G.,
 RA Hugot J.-P.;
 RT "CARD15 mutations in Blau syndrome.";
 RL Nat. Genet. 29:19-20(2001).
 CC -1- FUNCTION: Induces NF-kappaB via RICK (CARD14K, RIP2) and IKK-
 CC gamma. Confers responsiveness to intracellular bacterial
 CC lipopolysaccharides (LPS).
 CC -1- SUBUNIT: Binds to RICK by CARD-CARD interaction.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative initiation;
 CC Comment=2 isoforms, 1/Nod2 (shown here) and 2/Nod2b, are
 CC produced by alternative initiation. Both isoforms can activate
 CC NF-kappaB. Isoform 1 is more abundant.
 CC -1- TISSUE SPECIFICITY: Monocytes-specific.
 CC -1- DISEASE: Defects in CARD15 are the cause of Blau syndrome (BS)
 CC [MIM:186580], a rare autosomal dominant disorder characterized by
 CC early-onset granulomatous arthritis, uveitis and skin rash.
 CC Crohn's disease (CD) [MIM:266600], a form of remitting
 CC inflammatory bowel disease. CD may involve any part of the
 CC gastrointestinal tract, but most frequently the terminal ileum and
 CC colon. Bowel inflammation is transmural and discontinuous. Crohn's
 CC disease is commonly classified as autoimmune disease.
 CC -1- DISEASE: Defects in CARD15 are a cause of susceptibility to
 CC ulcerative colitis [MIM:191390], a chronic inflammatory bowel
 CC disease. In ulcerative colitis, the inflammation is continuous and
 CC limited to rectal and colonic mucosal layers. Ulcerative colitis
 CC is commonly classified as autoimmune disease.
 CC -1- SIMILARITY: Contains 2 CARD domains.

CC -1- SIMILARITY: Contains 1 NACHT domain.
 CC -1- SIMILARITY: Contains 6 leucine-rich (LRR) repeats.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL AF178930; AAC33677.1; -
 CC EMBL AF385089; AAK70867.1; -
 CC EMBL AF385090; AAK70868.1; -
 CC EMBL AJ103140; CAC42117.1; -
 CC Genem; H86C5331; CARD15.
 CC MIM; 603936; -
 CC MIM; 166580; -
 CC MIM; 266600; -
 CC MIM; 191390; -
 CC InterPro; IPR001315; CARD.
 CC InterPro; IPR001611; LRR.
 CC InterPro; IPR007091; LRR_NIMH.
 CC Pfam; PF00560; LRR; 2.
 CC SMART; SM00114; CARD; 1.
 CC PROSITE; PSS0209; CARD; 1.
 CC PROSITE; PSS0837; NACHT; 1.
 CC ATP-binding; Repeat; leucine-rich repeat; Disease mutation;
 CC Alternative initiation; Polymorphism.
 CC CHAIN 1 1040
 FT CASPASE RECRUITMENT DOMAIN PROTEIN 15,
 FT ISOFORM 1.
 FT CASPASE RECRUITMENT DOMAIN PROTEIN 15,
 FT ISOFORM 2.
 FT INIT MET 28 26
 FT DOMAIN 26 122
 FT DOMAIN 126 218
 FT DOMAIN 293 618
 FT NP_BIND 299 306
 FT REPEAT 786 812
 FT REPEAT 814 837
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 FT REPEAT 928 949
 FT REPEAT 954 977
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 FT VARIANT 140 140
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 FT VARIANT 189 189
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 FT /FTid=VAR_012665.
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 FT /FTid=VAR_012668.
 FT /FTid=VAR_012669.
 FT /FTid=VAR_012670.

FT	VARIANT	289	289	N -> S.
FT	VARIANT	291	291	/FTid=VAR_012671.
FT	VARIANT	291	291	D -> N (in CD).
FT	VARIANT	294	294	/FTid=VAR_012672.
FT	VARIANT	294	294	T -> S (in CD).
FT	VARIANT	301	301	/FTid=VAR_012673.
FT	VARIANT	301	301	A -> V (in CD).
FT	VARIANT	311	311	/FTid=VAR_012674.
FT	VARIANT	311	311	R -> W (in CD and ulcerative colitis).
FT	VARIANT	334	334	/FTid=VAR_012675.
FT	VARIANT	334	334	R -> Q (in BS).
FT	VARIANT	334	334	/FTid=VAR_012676.
FT	VARIANT	334	334	R -> W (in BS).
FT	VARIANT	348	348	/FTid=VAR_012677.
FT	VARIANT	348	348	L -> V (in CD).
FT	VARIANT	352	352	/FTid=VAR_012678.
FT	VARIANT	352	352	H -> R (in CD).
FT	VARIANT	373	373	/FTid=VAR_012679.
FT	VARIANT	373	373	R -> C (in CD).
FT	VARIANT	414	414	/FTid=VAR_012680.
FT	VARIANT	414	414	N -> S (in CD).
FT	VARIANT	431	431	/FTid=VAR_012681.
FT	VARIANT	431	431	S -> L (in CD).
FT	VARIANT	432	432	/FTid=VAR_012682.
FT	VARIANT	432	432	A -> V (in CD).
FT	VARIANT	441	441	/FTid=VAR_012683.
FT	VARIANT	441	441	E -> K (in CD).
FT	VARIANT	469	469	/FTid=VAR_012684.
FT	VARIANT	469	469	L -> F (in BS).
FT	VARIANT	612	612	/FTid=VAR_012685.
FT	VARIANT	612	612	A -> T (in CD).
FT	VARIANT	612	612	/FTid=VAR_012686.
FT	VARIANT	684	684	A -> V (in CD).
FT	VARIANT	684	684	/FTid=VAR_012687.
FT	VARIANT	702	702	R -> W (in CD).
FT	VARIANT	702	702	/FTid=VAR_012688.
FT	VARIANT	703	703	R -> W (risk factor for CD).
FT	VARIANT	703	703	/FTid=VAR_012689.
FT	VARIANT	713	713	R -> C (in CD and ulcerative colitis).
FT	VARIANT	713	713	/FTid=VAR_012690.
FT	VARIANT	725	725	R -> C (in CD).
FT	VARIANT	725	725	/FTid=VAR_012691.
FT	VARIANT	755	755	A -> G (in CD).
FT	VARIANT	755	755	/FTid=VAR_012692.
FT	VARIANT	758	758	A -> V (in CD and ulcerative colitis).
FT	VARIANT	758	758	/FTid=VAR_012693.
FT	VARIANT	778	778	A -> V (in CD).
FT	VARIANT	778	778	E -> K (in CD).
FT	VARIANT	793	793	/FTid=VAR_012694.
FT	VARIANT	793	793	E -> K (in CD).
FT	VARIANT	843	843	/FTid=VAR_012695.
FT	VARIANT	843	843	V -> M (in CD).
FT	VARIANT	853	853	E -> K (in CD).
FT	VARIANT	853	853	/FTid=VAR_012697.
FT	VARIANT	863	863	N -> S (in CD).
FT	VARIANT	863	863	/FTid=VAR_012698.
FT	VARIANT	863	863	M -> V (in CD).

FT	VARIANT	885	885	/FTid=VAR_012699.
FT	VARIANT	885	885	A -> T (in ulcerative colitis).
FT	VARIANT	908	908	/FTid=VAR_012700.
FT	VARIANT	908	908	G -> R (in CD).
FT	VARIANT	918	918	/FTid=VAR_012701.
FT	VARIANT	918	918	A -> D (risk factor for CD).
FT	VARIANT	924	924	/FTid=VAR_012702.
FT	VARIANT	924	924	G -> D (in CD).
FT	VARIANT	955	955	/FTid=VAR_012703.
FT	VARIANT	955	955	V -> I.
FT	MUTAGEN	305	305	/FTid=VAR_012704.
FT	MUTAGEN	305	305	K -> R: NO ACTIVATION.
FT	SEQUENCE	1040 AA; 115282 MW; 0037592D96DDDF CRC64;		

Alignment Scores:

Pred. No.:	2.85e-267	Length:	1040
Score:	5448.00	Matches:	1040
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	65.88%	Indels:	0
DB:	1	Gaps:	0

US-10-014-269-1 (1-4485) x CARF_HUMAN (1-1040)

QY	106	ATGAGGGAAGAGGCTGTTCAAGCTCTACAGATAGAGAGAAAGACAGATGCTCTC	165
DB	1	MetGlyGluGluGlySerAlaSerHisAspGluGluAlaGlnAlaSerValLeuLeu	20
QY	166	GGACATCTCCGGGTGTGAAATGCTCGAGAGAGCTTTTACGACAGAGAGCGC	225
DB	21	GlyHisSerProGlyGluMetCysSerGlnAlaPheGlnAlaGlnIleSerGln	40
QY	226	CTGGTGAAGCTGCTGCTCAGAGGCTCCCTGAGAGGCTTCGAGATGTCGACTGCTG	285
DB	41	LeuValGluLeuLeuValSerGlySerLeuGluGlnPheGluSerValLeuAspTyrLeu	60
QY	286	CTGCTCGAGAGCTCTCTCTCGAGAGACTACAGAGGCTTCACCTCTGAGCGACGCT	345
DB	61	LeuSerTyrGluValLeuSerTyrGluAspTyrGluGlyPheHisLeuLeuGlnPro	80
QY	346	CTCTCCCACTTGGCCAGGCGCTTTCGACACGCTCGAATTAAGGCTTGGGCTGT	405
DB	81	LeuSerHisLeuAlaArgAlaGluLeuAspThrValTyrAsnGlySerTyrPalaCys	100
QY	406	CAGAGCTCATCGCGCTGCCAAGAACCCAGGCCGACACAGCAATGCCCCAGCTCAT	465
DB	101	GlnGlyLeuIleAlaAlaGlnGluAlaGlnAlaAspSerGlnSerProGlyLeuHis	120
QY	466	GGCTGCTGGACCCCACTGCTCCACCCAGCCGAGCTCGAGAGTCAACCGGCGACGC	525
DB	121	GlyCysTyrAspProHisSerLeuHisProLysArgAspLeuGlnSerHisArgProAla	140
QY	526	ATTGTCAAGAGGCTCCACAGCAATGTGAGAACTGTCGACTGGCATGGAGCGGCT	585
DB	141	IleValArgArgLeuHisSerHisValGluAsnMetLeuAspLeuAlaTyrPalaGly	160
QY	586	TTCGTACACCAAGATGAAATGTGATGAATTCAGGTCCGATCTTCAACCGCTCCACAG	645

Db	161	PheValSerClnTyrGluCysAspIleIleHLeuProlLeuPheThrProSerGlnArg	180	Db	441	GluPheLeuLeuLysGlyPheSerGluGlnGlyIleGluLeuTyrLeuArgLysAlaGln	460
QY	646	GCAAGAAAGGCTGCTTGATCTTCACCAACGGTGAAGGAAAGGATGGCTGGCTTCCTCTA	705	QY	1486	CATGAACCCGGGCTGGAGAACCGCTCATCCGCGCTGCTCAAGAACCTCAAGCCCTGCAC	1545
Db	181	AlaArgArgLeuLeuAspLeuAlaThrValLysAlaAsnGlyLeuAlaAlaPheLeuLeu	200	Db	461	HisGluProGlyValAlaAspArgLeuLeuLeuArgLeuGlnGlnGlnThrSerAlaLeuHis	480
QY	706	CACATGTTCAAGAAATACCACTCCCATTTGGCCCTGGCTTGGAAAGCTGCACATGCAAG	765	QY	1546	GGTTTGCAACCTGGCTGTCTCTACAGAAATGGTGTCCAAATGCCAACGAAATCTGTG	1605
Db	201	GlnHisValGlnGlnLeuProlArgProlLeuAlaLeuProlGlnAlaAlaThrCysLys	220	Db	481	GlyLeuCysHisLeuProlValPheSerThrPheValSerLysCysHisSerGlnLeuLeu	500
QY	766	AAGTATATGGCCAAAGCTGAGAACCAACGGTGTCTGCTCACTGGCTTCCTCACTACCTAT	825	QY	1606	CTGCAGAGAGGGGGGGTCCCAAAAGCACTACAAATATGTACCTGATTCCTCAAGCAT	1665
Db	221	LysTyrMetAlaLysLeuArgThrThrValSerAlaGlnSerArgPheLeuSerThrTyr	240	Db	501	LeuGlnGlnGlnGlySerProLysThrThrThrAspMetTyrLeuLeuLeuGlnHis	520
QY	826	GATGAGACAGACGCTGCTGGAGAACATATACAGAAATGTCTGGAGGCTCTGG	885	QY	1666	TTTCCTGCTGCATGCAACCCCGCCAGACTCACTCTCCCAAGGTCTGGAGCCCACTTCTT	1725
Db	241	AspGlyAlaGlnThrLeuCysLeuGlnAspIleTyrThrLeuAsnValLeuGlnValTyr	260	Db	521	PheLeuLeuHisAlaThrProProAspSerAlaSerGlnGlyLeuGlyProSerLeuLeu	540
QY	886	GCAAGATGTGGGCAATGAGTGGACCCGCCAGAAAGACCCAGCCACTGGAGCTGGAGAG	945	QY	1726	CGGGGCCGCGCTCCCAACCTCCTGCACCTGGGCAAGACTGGCTGTGGGGCTGGCATG	1785
Db	261	AlaAspValGlyMetAlaGlyProProGlnLysSerProAlaThrLeuGlyLeuGln	280	Db	541	ArgGlyArgLeuProlThrLeuLeuHisLeuGlyArgLeuAlaLeuTyrPylLeuGlyMet	560
QY	946	CTCTGACGACCCCTGGCCACCTCAATGACATGGCGACACTGTGCTGGTGGTGGTGGAG	1005	QY	1786	TGCTGCTACGTGTCTCAGCCAGCACTCCAGGCAACAGGTCAAGCCCTGATGACATT	1845
Db	281	LeuPheSerThrProGlyHisLeuAsnAspAlaAspThrValLeuValValGlyGln	300	Db	561	CysCysTyrValPheSerAlaGlnGlnLeuGlnAlaAlaGlnValSerProAspAspIle	580
QY	1006	GCGGGCAGTGGCAAGACAGCAGCTCTGACAGCGGCTGCACCTGCTGTGGGCTGCAGGCAA	1065	QY	1846	TCCTTGCTGCTGCTGGTGGTGGCAAGGTGTGGTGGAGGAGTACGGCCCGCTGAA	1905
Db	301	AlaGlySerGlyLysSerThrLeuLeuGlnHArgLeuHisLeuLeuThrPylAlaGlyGln	320	Db	581	SerLeuGlnPheLeuValArgAlaLysGlyValAlaProGlySerThrAlaProlLeuGln	600
QY	1066	GACTCCAGGAATTTCTCTTTGTCTTCCCATTCAGCTGCCGGACAGCTGCAGTGCATGGCC	1125	QY	1906	TTCTTTCAACATCACTTTCAAGTGTCTTTTGGCGGTTCCTACCTGGCACTCAAGTCAAT	1965
Db	321	AspPheGlnGlnPheLeuPheValPheProPheSerCysArgGlnLeuGlnCysMetAla	340	Db	601	PheLeuHisIleThrPheGlnCysPhePheAlaAlaPheTyrLeuAlaLeuSerAlaAsp	620
QY	1126	AAACACCTCTCTGGCGGAGCTACTCTTTAGACACTGCTGTGGGCTGATGTGATCAA	1185	QY	1966	GTCCACACAGCTTGTCTCAACAACCTCTCAATTGGAGAGGCAAGCACTCAACCAAG	2025
Db	341	LysProlLeuSerValArgThrLeuLeuPheGlnHisCysCysTyrProAspValGlyGln	360	Db	621	ValProProlAlaLeuLeuArgHisLeuPheAsnCysGlyArgProGlyLysAsnSerProMet	640
QY	1186	GAAAGACATCTTCCAGTTACTCCTTGACCAACCTGACCGTGTCTTAACTTTGATGGC	1245	QY	2026	GCCAAGCTCCTGCCACAGATGTGCATCCAGGCGCTCGAGAGGAAAGACACAGAGGTGGCA	2085
Db	361	GluAspIlePheGlnLeuLeuLeuAspHisProAspArgValLeuLeuThrPheAspGly	380	Db	641	AlaArgLeuLeuProlThrMetCysIleGlnAlaSerGlnGlyLysAspSerSerValAla	660
QY	1246	TTTGACGAGTTCAAGTTCAAGTTCAAGTATGTGAAAGCACTGTCCTCCCGACCGACCC	1305	QY	2086	GCTTTCGCTGCAGAAAGGCCAGCCGACCAACCTTCAGATCAAGCAAGCCTCTCTGGACGAG	2145
Db	381	PheAspGluPheLysPheArgPheThrAspArgGlnArgHisCysSerProThrAspPro	400	Db	661	AlaLeuLeuGlnLysAlaGluProHisAsnLeuGlnIleThrAlaAlaPheLeuAlaGly	680
QY	1306	ACCTGTGTCAAGACCTGCTCTTCAACCTTTCGAGGAGCAACCTGCTGAAGAAATGCCCGC	1365	QY	2146	CTGTGTCCCGGAGCACTGGGGCGCTGCTGGCTGAGTGGCAACATCTGAGAAGCCCGT	2205
Db	401	ThrSerValGlnThrLeuLeuPheLeuLeuGlnGlnLysAsnLeuLysAsnAlaArg	420	Db	681	LeuLeuSerArgGlnHisTyrPylLeuLeuAlaGlnCysGlnThrSerGlnLysAlaLeu	700
QY	1366	AAAGGTGTGCACAGCCGCTCCGGCCGCTGTGTGGCGCTTCTTCAAGAAAGTACCTCCGAC	1425	QY	2206	CTCCGGCCCAAGCCTGTGCCCGCTGGTGTCTGAGCCCGACACTCCGCAAGCACTTCAC	2265
Db	421	LysValValThrSerArgProAlaAlaValSerAlaPheLeuArgLysTyrIleArgThr	440	Db	701	LeuArgArgGlnIleCysAlaArgTyrCysLeuAlaArgSerLeuArgLysHisPheHis	720
QY	1426	GAGTTCACCTCAAGGGCTTCTCTGAACAGGCACTGACGTGTACTGAGGAAGCGCAAT	1485	QY	2266	TCCATCCCGGCACTGCACCGGGGTGAGGCCAAGAGGTGCATGGCATGGCCGGGTTCAAT	2325
				Db	721	SerIleProProlAlaIleProGlyGlnAlaLysSerValHisAlaMetProGlyPheIle	740

QY 2326 TGGCTCATCCGAGGCTGTACAGATGCAAGAGAGGCGCTGGCTGGAAAGCTGCACT 2385
 DB 741 Trrpleuilear9serLeuTr9gluWetGlnluLugluLeuAlaAArg 760
 QY 2386 GGCCCTGATGTTGGGCACTCAAGTTCATTTTGCAGTGTGGGCCCCCATGAGTGTCT 2445
 DB 761 GlyLeuAsnValGlyHisLeuLysLeuThrPheCysSerValGlyProthrGluGlyAla 760
 QY 2446 GCCCTGGCTTTGTGTGCGACGACCTCCGCGCGCCCTGGCCCTGCGAGTGAAC 2505
 DB 781 AlaLeuAlaPheValLeuGlnHisLeuArgArgProValAlaLeuGlnLeuAspTyrAsn 800
 QY 2506 TCTGTGGGTGACATTGGCGGTGAGACGCTGCTGCCCTTGGCTGTGTCTGCAAGGCTCTG 2565
 DB 801 SerValGlyAspIleGlyValGluGlnLeuLeuProCysLeuGlyValCysLysAlaLeu 820
 QY 2566 TATTGGCGCATTAACAAATCTCAGACCCAGGCACTTGCACAGCTCATGATGTCTCTT 2625
 DB 821 TyrLeuArgAspAsnAsnIleSerAspArgGlyIleCysLysLeuIleGluCysAlaLeu 840
 QY 2626 CACTCGGACCAATTGCGAAGTGTGCTTATCAACAACAATTGACTGACGCGCTGGCA 2685
 DB 841 HisCysGluGlnLeuGlnLysLeuAlaLeuPheAsnAsnLysLeuThrAspGlyCysAla 860
 QY 2686 CACTCCATGGCTAAAGCTCTTGCATGCAAGGCAAACTCTTGGCATTTGAGGCTTGGGGAAT 2745
 DB 861 HisSerMetAlaLysLeuLeuAlaCysArgGlnAsnPheLeuAlaLeuArgLeuGlyAsn 880
 QY 2746 AACCTACATGATGCGCGGAGAGCCCAAGTGTGGCGGAGGCGCTCCGAGGCAACACTCC 2805
 DB 881 AsnTyrIleThrAlaAlaGlyAlaGlnValLeuAlaGluGlyLeuArgGlyAsnThrSer 900
 QY 2806 TTGCAATTCCTGGGATTCGTGGGGCCAAAGAGTGGGTGAGAGGGGGCCAGGCCCTG 2865
 DB 901 LeuGlnPheLeuGlnGlyPheTrpGlyAsnArgValGlyAspGluGlyAlaGlnAlaLeuAla 920
 QY 2866 GAAAGCTTGGTGTATCACAAGAGCTTGAAGTGGCTCAAGCTGTGGGGAACAACATTGGC 2925
 DB 921 GluAlaLeuGlnLysPheIleSerLeuArgTrpLeuSerLeuValGlyAsnAsnIleGly 940
 QY 2926 AGTGTGGTGGCCAAAGCTTGGCACTGATGCTGGCAAAAGAGCTCATGCTTGAAGAACTC 2985
 DB 941 SerValGlyAlaGlnAlaLeuAlaLeuMetLeuAlaLysAsnValMetLeuGluGluLeu 960
 QY 2986 TGGCTGAGAGAGAACATCTCAAGATGAAGTGTATGTTCTCTGCAAGAGAGCTGAG 3045
 DB 961 CysLeuGluGluLysAsnHisLeuGlnAspGluGlyValCysSerLeuAlaGluGlyLeuLys 980
 QY 3046 AAAAATTCAGTTGAAAATCCTGAAGTTGTCCAAATACCTGCATCACCTACCTAGGGGGA 3105
 DB 981 LysAsnSerSerLeuLysIleLeuLysLeuSerAsnAsnCysIleThrTyrIleGlyAla 1000
 QY 3106 GAAAGCTTCTGCAAGGCGCTTGAAGAGATGACACCATCTTGAGAGTCTGGCTCGAGGG 3165
 DB 1001 GluAlaLeuLeuGlnAlaLeuGlnLysAsnAspThrIleLeuGlnValIrrpleuAspGly 1020

QY 3166 AACACTTTCCTCTACAGAGAGGATTGACAAAGCTCGAGGAGACACAGACTTCTGCTT 3225
 DB 1021 AsnThrPheSerLeuGlnLugluValAspLysLeuGluCysArgAspThrArgLeuLeu 1040

RESULT 2
 ID CARF MOUSE STANDARD; PRT; 1020 AA.
 AC Q8K3ZF0.
 DT 15-SEP-2003 (Rel. 42, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Caspase recruitment domain protein 15 (Nod2 protein).
 GN CARD15 OR NOD2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=BALE/c; TISSUE=Monocytes;
 RA Itanaga Y., Davey M.P., Martin T.M., Planck S.R., DePriest M.L.,
 RA Baugh M.M., Suing C., Rosenbaum J.T.;
 RT "Cloning, sequencing and expression analysis of the murine Nod2/CARD15
 RT gene.";
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 RN (2)
 RP SEQUENCE FROM N.A. (ISOFORM 2), AND VARIANTS ALA-212; ARG-240;
 RP CYS-422; VAL-485; ALA-603; ILE-675 AND GLN-925.
 RC STRAIN=NR1; TISSUE=Breast cancer;
 RX MEDLINE=22389297; Pubmed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.U., Ueda T.B., Tomshyuk S., Carninci P., Prange C.,
 RA Rhee S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Basak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Halysk S.W.,
 RA Villalón D.R., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahay J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Induces NF-kappaB via RICK (CARD14, RIP2) and IKK-
 CC gamma. Confers responsiveness to intracellular bacterial
 CC lipopolysaccharides (LPS) (By similarity).
 CC -!- SUBUNIT: Binds to RICK by CARD-CARD interaction (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;

[illegible]

Db 246 AlaGlyAlaLeuGlnLysSerProAlaIleLeuGlnLeuAlaPheLeuPheSerThrHis 265
QY 961 GGCCACCTCAATGACGATGGGACACATGTGTGCTGGTGGGTGAAGGCGGACAGTGGCAAG 1020
Db 266 GlyHisLeuAsnArgAspAlaSerThrIleLeuValAlaGlnAlaGlySerGlyLeu 285
QY 1021 AGCAGCTCTCTGACAGGGGCTGCACTGTGTGTGGCTGACAGGGCAAGACTTCCAGAAATT 1080
Db 286 SerThrLeuGlnAlaLeuHisLeuLeuThrAlaThrGlyAlaSerPheGlnAlaPhe 305
QY 1081 CTCTTTGTCTTCCCATTCAGCTGCCGGACAGCTGAGTGGCAACCAACTCTGTG 1140
Db 306 LeuPheIlePheProPheSerCysArgGlnLeuGlnCysValAlaLysProLeuSerLeu 325
QY 1141 CGACCTACTCTTTGAGCACTGGCTGTGGCCTGATGTGTGTCAAGAAAGACTTCCAG 1200
Db 326 ArgThrLeuLeuPheGlnHisCysCysTrpProAspValAlaGlnAspAspValPheGln 345
QY 1201 TTACTCTTGACCACTGACCGGTGCTCTTAACTTTGATGGCTTGACAGATTCAAG 1260
Db 346 PheLeuLeuAspHisProAspArgValLeuLeuThrPheAspGlyLeuAspGluPheLys 365
QY 1261 TTCAGGTTACGGATCGTGAAGCCACTGCTCCCGACCGACCCCACTCTGTCAATC 1320
Db 366 PheArgPheThrAspArgGlnArgHisCysSerProIleAspProThrSerValGlnThr 385
QY 1321 CTGCTCTTCAACTCTTGACGAGGACCACTGCTGAAAGATGCCCGCAAGGTGTACCAAG 1380
Db 386 LeuLeuPheAsnLeuLeuGlnGlyAsnLeuLeuLysAsnHisCysLysValLeuThrSer 405
QY 1381 CGTCCGCGCCTGTGTGCGCTTCCAGAAAGTACATCCGACCAAGTTCAACTCAAG 1440
Db 406 ArgProAspAlaValSerAlaLeuLeuArgLysPheValArgThrLeuGlnLeuLys 425
QY 1441 GGCTCTTGAAAGGGGACATGCACTGTACTGAGAGAGCGGCATCATGAGCCGCGGGTG 1500
Db 426 GlyPheSerGlnGlnGlyIleGlnLeuTyrLeuArgLysHisHisArgGluProGlyVal 445
QY 1501 GCGAAGCGCTCATCCGCTGCTCCAAAGAGACTGACCCCTCAAGGTTGTGGCACTG 1560
Db 446 AlaAspArgLeuIleGlnLeuIleGlnAlaThrSerAlaLeuHisSerGlyLeuCysHisLeu 465
QY 1561 CTGTCTCTCATGATGATGTCATATGCCACAGAACTGTGCTGCAAGGAGGGGAG 1620
Db 466 ProValPheSerTrpPheValSerArgCysHisArgLeuLeuLeuGlnAsnArgGly 485
QY 1621 TCCCAAAAGACACTACAGATATGTAOCTGCTGATTCGACAGATTTCGTGCAATGC 1680
Db 486 PheProThrThrThrSerThrAspMetTyrLeuLeuIleLeuGlnHisPheLeuLeuHisAla 505
QY 1681 AOCOCOCACAGACTTCCCAAGGCTGGGAGCCAGGCTTCTGGGAGCGGCTCCCC 1740
Db 506 SerProProAspSerSerProLeuGlnLysLeuGlyProGlyLeuLeuHisSerTyrLeuSer 525
QY 1741 AOCCTCTGACACTGGGACAGACTGGCTGTGTGGGCGCTGGGCACTGTGCTGCACTGTTC 1800

Db 526 ThrLeuLeuHisLeuGlnHisLeuAlaLeuArgGlyLeuAlaLeuSerCysTyrValPhe 545
QY 1801 TCAGCCCAAGACTCCAGGACAGCAGGCTGACCCCTGATGACATTTCTTGGCTCCG 1860
Db 546 SerAlaGlnGlnLeuGlnAlaAlaGlnValAspSerThrAspArgIleSerLeuGlyPheLeu 565
QY 1861 GTCCGTGCCAAAGGTGTGTCGACAGGAGTACGGGCGCCCTGAAATTCCTTCAACACT 1920
Db 566 ValArgAlaGlnSerSerValProGlySerLysAlaProLeuGluPheLeuHisIleThr 585
QY 1921 TTCAGTGCCTCTTTCGCGGCTTCACTGCGCACTCAGTGGCTGATGGCCACCACTTGG 1980
Db 586 PheGlnCysPhePheAlaAlaPheTyrLeuAlaValSerAlaAspHisSerValAlaSer 605
QY 1981 CTACAGACCTCTTCAATTTGGAGAGGCGCACTCAACATGGCAAGGCTCTGCC 2040
Db 606 LeuLysHisLeuPheSerCysGlyArgLeuLysSerSerLeuLeuGlyArgLeuLeuPro 625
QY 2041 ACAGTGTCACTCCAGGCGCTCCGAGGGAAGAGACAGAGCGGTGGCAGCTTGTGCAAG 2100
Db 626 AsnLeuCysIleGlnGlnLysSerArgValLysLysGlySerGluAlaAlaLeuLeuGlnLys 645
QY 2101 GCGAAGCCGCAACCTTCAGATCAAGACACCTTCCTGGAGGCTGTGTCCCGAG 2160
Db 646 AlaGluProHisAsnLeuGlnIleThrAlaAlaPheLeuAlaGlyLeuLeuSerGlnGln 665
QY 2161 CACTGGGCGCTGCTGGCTGAGTGCAGACATCTGAGAGAGCCCTGCTCCGCGGCAAGCC 2220
Db 666 HisArgAspLeuLeuAlaAlaCysGlnValSerLeuValLeuLeuAlaArgGlnAla 685
QY 2221 TGTGCCCGCTGTGTGTGCGCGCACCTCCGACAGCACTTCACATCCCGCAGCT 2280
Db 686 ArgAlaArgSerCysLeuAlaHisSerLeuLysGlnHisSerHisSerIleProProAla 705
QY 2281 GCACGGGCTGAGGCGCAAGAGCTGCATGCATGCCCGGCTCATCTGGCTCATCCGAGC 2340
Db 706 ValProGlyAluThrLysSerPheHisAlaSerProGlyPheIleTrpLeuIleArgSer 725
QY 2341 CTGTACAGATGCAAGAGAGAGCGGCTGGCTGCGAAGCTGCGACGTCGATGATGTGG 2400
Db 726 LeuTyrGlnLysGlnGlnGlnGlnLeuAlaGlnAlaValaArgLysLeuAspIleGly 745
QY 2401 CACTCAAGTTGACATTTGCACTGTGGGCGCCACTGAGTGTGCTGCCCTGGCTTGTG 2460
Db 746 HisLeuLysLeuThrPheCysArgValGlyProAlaGlnCysAlaAlaLeuAlaPheVal 765
QY 2461 CTCAGACACTCCGCGCGCGCTGGCCCTGCACTGCACTCAACTCTGTGGGTGACAT 2520
Db 766 LeuGlnHisLeuGlnArgProValAlaLeuGlnLeuAspTyrAsnSerValGlyAspVal 785
QY 2521 GCGTGAAGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2580
Db 786 GlyValGlnGlnLeuArgProCysLeuGlyValCysThrAlaLeuTyrLeuAlaGlyAsn 805
QY 2581 AATATCTCAAGCCAGGAGCTGCAAGGCTCATGATGATGCTGCTGCTGCGAGCAATG 2640
Db 806 AsnIleSerAspArgGlyAlaArgThrLeuValGlnCysAlaLeuArgCysGlnGlnLeu 825

QY 2641 CAGAGTTAGCTTATTCACAAATTCAGTCTGACACCTGCTCACTGGCTAAG 2700
 Db 826 GlnysLeuAlaLeuPheAsnAsnLysLeuThrPalaCysAlaCysSerMetAlaLys 845
 QY 2701 CTCTTCATGAGGCAAACTTCCTGGCAATTGAGGCTGGGGAATAACTCATCTACCTGCC 2760
 Db 846 LeuLeuAlaHisLysGlnAsnPheLeuSerLeuValGlyAsnAsnHisLeuAla 865
 QY 2761 GCGGAGCCCAAGTGTGCGCAAGGCTCCAGGCAACCTCTCTGCAATTGCTGGCA 2820
 Db 866 AlaGlyAlaGluValLeuAlaGlnGlyLysSerAsnThrSerLeuLysPheLeuGly 885
 QY 2821 TTCTGGGCAACAGAGTGGGTGAGAGGAGGCGCTGAGAGCTGAGAGCTTGGGTGAT 2880
 Db 886 PheTrpGlyAsnSerValGlyAspLysGlyThrGlnAlaLeuAlaGluValAlaAsp 905
 QY 2881 CACCAAGCTTGAAGTGGCTCAGGCTGGTGGGAAACAATTGGCAGTGGGTGCCCA 2940
 Db 906 HisGlnAsnLeuLysTrpLeuSerLeuValGlyAsnAsnLysGlySerMetGlyAlaGlu 925
 QY 2941 GCGTTGCACTGATGCTGGCAAGACACTGACAGAACTCTGCTGAGAGAGAAC 3000
 Db 926 AlaLeuAlaLeuLeuLeuGlnLysSerLeuGlnLysLeuGlnLysLeuGlnLys 945
 QY 3001 CATCTCCAGATGAAGTGTATGTTCTCTGCAAGAGACTGAGAAATTCAGATTG 3060
 Db 946 HisLeuCyAspGlnGlyValLysSerLeuAlaGlnLysLeuLysAspGlnSerThrLeu 965
 QY 3061 AAAATCCTGAAGTGTGCAATACTGCATCACTTACCTAGGGGCAAGAGCTCTGCA 3120
 Db 966 LysPheLeuLysLeuSerAsnAsnGlyLeuThrTyArgGlyAlaGluAlaLeuLeuGln 985
 QY 3121 GCGCTTGAAGGATGACACACTCTGCAAGCTGCGCTCCAGGGAACACTTCTCTCTA 3180
 Db 986 AlaLeuSerArgAsnSerAlaLeuGlnLysValTrpLeuArgGlyAsnThrPheSerLeu 1005
 QY 3181 GAGGAGGTTGACAAAGCTCGGCTGCAAGGACACAGACTCTCTCTT 3225
 Db 1006 GlnGluLeuGlnThrLeuSerSerArgAspAlaArgLeuLeuLeu 1020

Search completed: January 7, 2004, 19:42:15
 Job time : 424.746 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: January 7, 2004, 19:25:21 ; Search time 170.731 Seconds
 (without alignments)
 13537.774 Million cell updates/sec

Title: US-10-014-269-1
 Perfect score: 8270
 Sequence: 1 gtagagcagatccaggtccac.....ataaacgttgagtcacaac 4485

Scoring table:

	BLOSUM62	Xgapop 10.0	Xgapext 0.5
Ygapop 10.0			
Ygapop 6.0			
Delop 6.0			
Delop 7.0			

Searched: 830525 seqs, 256052604 residues

Total number of hits satisfying chosen parameters: 1661050

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 150 summaries

Command line parameters:
 -MODEL=frame+_n2p.model -DEV=slp
 -Q/cgn2_1/USP10.spool_p/US10014269/runat_07012004_175229_24521/app_query.fasta_1
 .3338
 -DB=SPTREMBL_23 -QFMT=fastan -SUFFIX=rspt -MINMATCH=0.1 -LOOPL=0 -LOOPEXT=0
 -UNITS=bits -START=1 -END=1 -MATRIX=blsum62 -TRANS=humand0.cdi -LIST=150
 -DOCLIGN=200 -THR SCORE=spct -THR MAX=100 -THR MIN=0 -ALIGN=50 -MODE=LOCAL
 -OUTFMT=ptc -NORW=ext -HEAPSIZE=500 -MINTEN=0 -MAXLEN=200000000
 -USER=US10014269.GCON.1.1.482.Gcnat.07012004.175229.24521 -NCP=6 -ICP=3
 -NO_MAP -LARGEOUTERY -NEG_SCORES=0 -WALT -DSFBLCK=100 -LONELOG
 -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : SPTREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*

11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvifus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match Length	ID	Description	41	300.5	3.6	1464	11	Q8BKX2	Q8BKX2 mus musculus
1	4196	50.7	1020 11	Q8K320	57	288.5	3.5	1447	13	Q91B91	Q91B91 xenopus lae
2	1222.5	14.8	953 11	Q8BH80	58	287.5	3.5	706	12	Q41972	Q41972 murid herpe
3	1209.5	14.6	953 4	Q81WFS	59	286.5	3.5	1418	6	Q28396	Q28396 equus caball
4	1019	12.3	706 11	Q8BUT6	60	286.5	3.5	2715	5	Q61603	Q61603 drosophila
5	505.5	6.1	1033 11	Q8R438	61	286	3.5	1669	11	Q9Q250	Q9Q250 mus musculus
6	483	5.8	892 4	Q8NEU4	62	286	3.5	4123	4	Q75851	Q9Q250 mus musculus
7	437	5.3	1052 7	Q8CUD8	63	286	3.5	4958	11	Q8CG65	Q8CG65 mus musculus
8	437	5.3	1073 7	Q8CUD8	64	285	3.5	2944	11	Q63870	Q63870 mus musculus
9	437	5.3	1153 7	Q9GJ50	65	284	3.4	223	4	Q8N102	Q8N102 homo sapien
10	425	5.1	1155 7	Q9PPE1	66	283.5	3.5	1626	4	Q8NFW1	Q8NFW1 homo sapien
11	410.5	5.0	778 4	Q8NFA8	67	283	3.4	1163	4	Q8NFW1	Q8NFW1 homo sapien
12	377.5	4.6	713 6	Q8NFA8	68	281.5	3.4	1664	6	Q8HVC1	Q8HVC1 homo sapien
13	365.5	4.4	499 4	Q8NFA8	69	281.5	3.4	2703	5	Q9VEG7	Q9VEG7 drosophila
14	360.5	4.4	982 11	Q8BUI4	70	281.5	3.4	4998	11	Q8CG65	Q8CG65 mus musculus
15	357.5	4.3	733 4	Q8IEE2	71	280.5	3.4	1414	5	Q26634	Q26634 strongyloce
16	353	4.3	5146 6	Q8SPM4	72	279.5	3.4	1419	11	Q63123	Q63123 rattus norv
17	350.5	4.2	1056 4	Q8NFA2	73	279	3.4	1745	4	Q9NZQ6	Q9NZQ6 homo sapien
18	338.5	4.1	5146 6	Q8SPM4	74	279	3.4	2716	5	Q8IN94	Q8IN94 drosophila
19	332	4.0	846 4	Q8IXT0	75	278.5	3.4	605	10	Q932V8	Q932V8 aradipops
20	329.5	4.0	1787 10	Q8M4X9	76	278	3.4	727	12	Q41973	Q41973 murid herpe
21	325	4.0	1464 11	Q8BIM4	77	278	3.4	1153	4	Q8B6U4	Q8B6U4 mus musculus
22	322	3.9	932 4	Q8BFL4	78	278	3.4	1442	11	Q62033	Q62033 mus musculus
23	321.5	3.9	660 4	Q8NFW1	79	277.5	3.4	1626	4	Q8NFW1	Q8NFW1 homo sapien
24	321	3.9	692 4	Q8NFW1	80	276.5	3.3	1420	13	Q9OW37	Q9OW37 gallus gall
25	319	3.9	884 7	Q26D51	81	276	3.4	1682	11	Q9QZ89	Q9QZ89 mus musculus
26	318	3.9	4123 4	Q75851	82	275.5	3.4	1442	11	Q62031	Q62031 mus musculus
27	317	3.9	1222 11	Q8K173	83	275.5	3.4	1459	11	Q62032	Q62032 mus musculus
28	314	3.8	863 11	Q8C6J9	84	274.5	3.3	1669	11	Q9Q250	Q9Q250 mus musculus
29	314	3.8	1464 11	Q8BKX2	85	274.5	3.3	1450	13	Q9Y1B4	Q9Y1B4 cyrops pyrr
30	313	3.8	1464 4	Q8NFA7	86	274.5	3.3	1580	11	Q8BLX7	Q8BLX7 mus musculus
31	311	3.8	1637 6	Q9XSV8	87	274.5	3.3	1682	11	Q9QZ89	Q9QZ89 mus musculus
32	310	3.8	1118 5	Q9YR13	88	274.5	3.3	1691	11	Q9ESQ2	Q9ESQ2 mus musculus
33	308.5	3.8	1461 4	Q76045	89	274	3.3	1497	11	Q61431	Q61431 mus musculus
34	308	3.8	1453 11	Q63079	90	273	3.3	195	4	Q8N101	Q8N101 homo sapien
35	307.5	3.7	977 7	Q8HNS9	91	273	3.3	1449	13	Q910C0	Q910C0 oncorhynch
36	307.5	3.7	1222 11	Q8K173	92	273	3.3	1802	5	Q17163	Q17163 brugia mala
37	307	3.7	1314 11	Q8CGA5	93	273	3.3	1820	13	Q91907	Q91907 parus major
38	305	3.7	397 11	Q8BUI4	94	272.5	3.3	1487	6	Q77753	Q77753 canis fami
39	304.5	3.7	1464 11	Q8BIM4	95	271.5	3.3	1418	6	Q28396	Q28396 equus caball
40	303	3.7	774 12	Q41971	96	271	3.3	1378	5	Q97405	Q97405 halictus di
					97	271	3.3	1840	11	Q91103	Q91103 rattus norv

98	270	3.3	1442	11	Q62031	Q62031 mus musculus
99	270	3.3	1442	11	Q62033	Q62033 mus musculus
100	270	3.3	1439	11	Q62032	Q62032 mus musculus
c 101	269.5	3.3	608	12	Q95K9	Q95K9 herpesvirus
102	269.5	3.3	1453	11	Q63079	Q63079 rattus norv
103	269.5	3.3	1461	4	Q76045	Q76045 homo sapien
104	269.5	3.3	1464	4	Q8N473	Q8N473 homo sapien
105	268	3.2	998	11	Q8CTM4	Q8CTM4 mus musculus
106	267.5	3.2	1487	4	Q14047	Q14047 homo sapien
c 107	267	3.3	1458	13	Q91089	Q91089 oncorhynch
c 108	264.5	3.2	1160	4	Q14046	Q14046 homo sapien
c 109	264.5	3.2	1352	13	Q90YU0	Q90YU0 brachydanio
c 110	264.5	3.2	1838	4	Q15094	Q15094 homo sapien
c 111	263	3.2	894	5	Q8WMS4	Q8WMS4 mytilus gal
112	263	3.2	1419	11	Q63123	Q63123 rattus norv
113	263	3.2	1838	11	Q88207	Q88207 mus musculus
114	262	3.2	1445	13	Q93251	Q93251 rana catesb
115	262	3.2	1447	13	Q91B91	Q91B91 xenopus lae
116	262	3.2	1737	11	Q9J104	Q9J104 rattus norv
117	262	3.2	1835	13	Q91A04	Q91A04 gallus gall
c 118	261.5	3.2	1449	13	Q91C00	Q91C00 oncorhynch
c 119	261	3.2	1827	13	Q8UND5	Q8UND5 cryzias lat
120	260	3.1	620	16	Q8XZM9	Q8XZM9 rickettsia s
c 121	259.5	3.2	1491	13	Q91718	Q91718 xenopus lae
c 122	259	3.2	998	11	Q8CTM4	Q8CTM4 mus musculus
c 123	259	3.2	1838	11	Q88207	Q88207 mus musculus
124	258.5	3.1	1621	4	Q9H4F9	Q9H4F9 homo sapien
c 125	258	3.1	1349	13	Q8AWI7	Q8AWI7 brachydanio
c 126	257.5	3.1	1684	6	Q8HVC1	Q8HVC1 canis famli
c 127	257.5	3.1	1739	11	Q9J1I2	Q9J1I2 mus musculus
128	257	3.1	1258	13	Q8AM11	Q8AM11 brachydanio
c 129	256.5	3.1	926	5	Q9W3G1	Q9W3G1 drosophila
130	256.5	3.1	1491	13	Q91718	Q91718 xenopus lae
131	256.5	3.1	1838	4	Q15094	Q15094 homo sapien
132	256.5	3.1	1840	11	Q9J103	Q9J103 rattus norv
133	255.5	3.1	888	13	Q90796	Q90796 gallus gall
c 134	255.5	3.1	1739	11	Q9J1I2	Q9J1I2 mus musculus
135	255	3.1	748	11	Q99KMO	Q99KMO mus musculus
136	254	3.1	1347	4	Q9EQB3	Q9EQB3 homo sapien
c 137	253	3.1	566	6	Q95JDI	Q95JDI sus scrofa
138	253	3.1	1840	11	Q60467	Q60467 cricetus
c 139	253	3.1	1840	11	Q60467	Q60467 cricetus
140	252.5	3.1	2703	5	Q9VEG7	Q9VEG7 drosophila
141	252.5	3.1	2715	5	Q61603	Q61603 drosophila
142	252.5	3.1	2716	5	Q8N84	Q8N84 drosophila
c 143	251.5	3.1	3084	12	Q8U211	Q8U211 pseudocaple
144	251	3.0	771	4	Q9JUC7	Q9JUC7 homo sapien
c 145	251	3.1	890	5	Q77087	Q77087 alvirella p
c 146	250.5	3.1	1258	13	Q8AWI1	Q8AWI1 brachydanio
c 147	250.5	3.1	563	5	Q981T5	Q981T5 nephila mad
c 148	250.5	3.1	685	6	Q9RTS5	Q9RTS5 bos taurus
149	250.5	3.0	817	5	Q964V6	Q964V6 dictyosteli
150	250.5	3.0	1366	4	Q15177	Q15177 homo sapien

ALIGNMENTS

QY	161	TGTGAATGTCCTCGACAGAGCTTTTCAGGACACAGAGGACCACTGGTGAAGTCTG	240
DB	6	CysaspketCysserClnGlnGlnuphGlnAlaGlnArgserGlnLeuValAlaLeuLeu	25
QY	241	GTCACAGGATCCTCGAGAGGCTTCAGAGTCTCGAGTGGTGGTCTCGGAGGTC	300
DB	26	IlseerGlsrleuslGlnGlnuphGlnAlaGlnArgserGlnLeuValAlaLeuLeu	45
QY	301	CTCTCCTGAGGAGTACAGAGGAGTTCACACTCTGGGACAGGCTCTCTCCACTTGGCC	360
DB	46	LeuserArgGlnuphGlnGlnuphGlnAlaGlnArgserGlnLeuValAlaLeuLeu	65
QY	361	AGGCGCTCTCGACACCGCTCTGATATAGGAGTACTGGGCTCTCTGAGACTCATCGG	420

QY	161	TGTGAATGTCCTCGACAGAGCTTTTCAGGACACAGAGGACCACTGGTGAAGTCTG	240
DB	6	CysaspketCysserClnGlnGlnuphGlnAlaGlnArgserGlnLeuValAlaLeuLeu	25
QY	241	GTCACAGGATCCTCGAGAGGCTTCAGAGTCTCGAGTGGTGGTCTCGGAGGTC	300
DB	26	IlseerGlsrleuslGlnGlnuphGlnAlaGlnArgserGlnLeuValAlaLeuLeu	45
QY	301	CTCTCCTGAGGAGTACAGAGGAGTTCACACTCTGGGACAGGCTCTCTCCACTTGGCC	360
DB	46	LeuserArgGlnuphGlnGlnuphGlnAlaGlnArgserGlnLeuValAlaLeuLeu	65
QY	361	AGGCGCTCTCGACACCGCTCTGATATAGGAGTACTGGGCTCTCTGAGACTCATCGG	420

QY	161	TGTGAATGTCCTCGACAGAGCTTTTCAGGACACAGAGGACCACTGGTGAAGTCTG	240
DB	6	CysaspketCysserClnGlnGlnuphGlnAlaGlnArgserGlnLeuValAlaLeuLeu	25
QY	241	GTCACAGGATCCTCGAGAGGCTTCAGAGTCTCGAGTGGTGGTCTCGGAGGTC	300
DB	26	IlseerGlsrleuslGlnGlnuphGlnAlaGlnArgserGlnLeuValAlaLeuLeu	45
QY	301	CTCTCCTGAGGAGTACAGAGGAGTTCACACTCTGGGACAGGCTCTCTCCACTTGGCC	360
DB	46	LeuserArgGlnuphGlnGlnuphGlnAlaGlnArgserGlnLeuValAlaLeuLeu	65
QY	361	AGGCGCTCTCGACACCGCTCTGATATAGGAGTACTGGGCTCTCTGAGACTCATCGG	420

Db 66 ArgArgLeuLeuAspThrValTrpAsnLysGlyValTrpLysGlyLeuLeuLeu 85
QY 421 GGTGCCCAAGAAAGCCGAGGCCACAGGCCAGTCCCAAGTGCATGGCTGCTGGACCCC 480
Db 86 AlaValGlnGlnAlaGlnAlaAsnSerHisThrPheGlnLeuLeuTyGlySerTrpAspThr 105
QY 481 CACTGGCTCCAGCCAGAGCCGAGAGCTGAGAGTCAAGCGGCAAGCCATTGTCAGAGAGCTC 540
Db 106 HisSerLeuHisProThrArgGlnSerHisSerHisSerProAlaLeuValArgArgLeu 125
QY 541 CACAGCCATGTGAGAAACATGCTGACCTGGCATGGAGGAGGAGTTTCGTCAGCCAGTAT 600
Db 126 TyrAsnHisValGlnAlaMetLeuGlnLeuAlaArgGlnGlyGlyPheLeuSerGlnTyr 145
QY 601 GATGTGATGAATCAGGTTGGCCATGCTCCACACCGCTCCCAAGGGGCAAGAGAGCTGTT 660
Db 146 GlucylGlnGlnLeuLeuArgLeuProLeuPheThrSerSerGlnArgAlaArgArgLeuLeu 165
QY 661 GATCTTGCCACGGTGAAAGCGAATGATGGCTGCTCTTCAACAATGTTCAAGAA 720
Db 166 AspLeuAlaValLysAlaAsnGlyLeuAlaAlaPheLeuLeuGlnHisValArgGln 185
QY 721 TTACAGTCCCATTTGGCCCTGGCTTGGAGGCTGCAATGCAGAAATATGGCCAA 780
Db 186 LeuProAlaProLeuProLeuProTyrGlnAlaAlaGlnGlyGlnLysPheLeuSerLys 205
QY 781 CTGAGGACCAAGGTGTCTGCTAGTCTCGTTCTCTCAATCAATATGATGAGACAGAG 840
Db 206 LeuArgThrMetValLeuThrGlnSerArgPheLeuSerThrTyrAspArgLysGlnAsn 225
QY 841 CTCTGCTGGAGACATATACAGAGAGATGTCTGAGAGTCTGGGAGCATGTGGGCA 900
Db 226 LeuLysLeuGlnAspLysIleTyrThrGlnAsnIleLeuLeuLeuGlnThrGlnValGlyThr 245
QY 901 GCTGGAACCCCGCAGAAAGCCAGCCAGCCCTGGGCTGAGAGAGCTCTTCAGACCCCT 960
Db 246 AlaGlyAlaLeuGlnLysSerProAlaIleLeuGlnLysLeuGlnAspLeuPheAspThrHis 265
QY 961 GGCCACCTCATGACATGCGGACACTGTGCTGGTGGTGGAGCGGCGCACTGGCCAA 1020
Db 266 GlyHisLeuAsnArgAspAlaAspThrIleLeuValValGlnGlnLysArgLysGlnLys 285
QY 1021 AGCAGCCTCTGACAGCGGCTGCACTTGTGTGGGCTGCAAGGCAAGCTTCCAGGAATT 1080
Db 286 SerThrLeuLeuGlnArgLeuHisLeuLeuTrpAlaHisGlyArgSerPheGlnGlnPhe 305
QY 1081 CTCTTTGCTTCCCATTCAGCTGCCGCGAGCTGCAATGTCATGGCCAAACCATCTCTG 1140
Db 306 LeuPheIlePheProPheSerCysArgGlnLeuGlnCysValAlaLysPheLeuSerLeu 325
QY 1141 CGGACTCTACTCTTGAGACATGCTGTGGCTGTATGTTGCTCAAGAAACATCTTCCAG 1200
Db 326 ArgThrLeuLeuPheGlnHisCysCysTrpProAspValAlaGlnAspAspValPheGln 345
QY 1201 TTACTCTTGAACACCTGACCGGTGCTCTGTTAATCTTGATGGCTTTCAGCAGTTCAAG 1260
Db 346 PheLeuLeuAspHisProAspArgValLeuLeuThrPheAspGlyLeuAspGlnPheLys 365

QY 1261 TTCAAGTTCAAGATGTTGAAGGCACTGCTCCCGGACCGAACCCCACTCTGTCCAGACC 1320
Db 366 PheArgPheThrAspArgGlnArgHisCysSerProIleAspProThrSerValGlnThr 385
QY 1321 CTGCTCTCAACCTCTGCAAGGCGCAACTGCTGAAGATCCCGCAAGAGTGGTACACAG 1380
Db 386 LeuLeuPheAsnLeuGlnGlnLysAsnLeuLeuLysAsnAlaCysLysValLeuThrHis 405
QY 1381 CGTCCGCGCGCTGTGTGCGGCTTCTCAAGAGATCATCCGACCAAGTCAACTCAAG 1440
Db 406 ArgProAspAlaValSerAlaLeuLeuArgLysPheValArgThrGlnLeuGlnLeuLys 425
QY 1441 GGCCTCTCAAGAGGCGATGAGAGCTGTAAGTCAAGAGACCGCATCATAGCCCGGAGT 1500
Db 426 GlyPheSerGlnGlnGlyLeuLeuLeuLeuArgLysHisSerGlnLysProGlyVal 445
QY 1501 GCGGACCGCTCATCCGCTGCTCCAGAGAGCTCAGCCCTGCAAGGTTTGTGCCACTG 1560
Db 446 AlaAspArgLeuIleGlnLeuIleGlnAlaThrSerAlaLeuHisGlnLysValLeuThr 465
QY 1561 CTGTCTCTCATGATGATGCTGCAATGCGACCAAGAACTGTTGCTGAGAGAGGAGG 1620
Db 466 ProValPheSerTrpMetValSerArgCysHisArgGlnLeuLeuGlnAsnArgGly 485
QY 1621 TCCCAAGAGACATACAGATATGTAAGTGTACCTGATCTGAGACATTTCTGCTCAATGCC 1680
Db 486 PheProThrHisSerThrAspMetLysLeuLeuIleLeuGlnHisPheLeuHisAla 505
QY 1681 ACCCCCGCAACTCAGCTTCCCAAGGCTGAGACCAAGTCTTCTGGGGGCGGCTCCCC 1740
Db 506 SerProProAspSerSerProLeuGlyLeuGlyProGlyLeuLeuGlnSerArgLeuSer 525
QY 1741 ACCCTGCTGCAACCTGGGCGAGACTGGCTGTGGGCGCTGGGCAATGTACAGTGTTC 1800
Db 526 ThrLeuHisLeuGlnHisLeuAlaLeuArgGlyLeuAlaMetSerCysTyrValPhe 545
QY 1801 TCAAGCCAGAGCTCCAGAGCAGCAGAGTCAAGCCCTGATGACATTTCTCTTGGCTTCTG 1860
Db 546 SerAlaGlnGlnLeuGlnAlaAlaGlnValAspSerAspAspLysSerLeuGlnPheLeu 565
QY 1861 GTGCTGTCMAAGTGTGTGCTGCCAGGAGTACGGGCGCCCTGCAATTCCTTCACATCACT 1920
Db 566 ValArgAlaGlnSerSerValProGlySerLysAlaProLeuGlnPheLeuHisIleThr 585
QY 1921 TTCCAGTCTTCTTGGCGGATTTCACTGGCACTCAGGCTGATGTGCACACAGCTTGG 1980
Db 586 PheGlnCysPhePheAlaAlaPheTyrLeuAlaValSerAlaAspThrSerValAlaSer 605
QY 1981 CTCACACACTCTTCAATGTGGCAGCCGCAAGCACTCAACCAATGCCAGGCTCTGCTGCC 2040
Db 606 LeuLysHisLeuPheSerCysGlyArgLeuGlnLysSerSerLeuLeuGlnValArgLeuLeuPro 625
QY 2041 ACCATGTGATCCAGGCGCTCGAGGGAAGAGCAGGCTGAGCACTTCTGCGCAAG 2100
Db 626 AsnLeuCysIleGlnLysSerArgValLysLysGlnSerGlnAlaLeuLeuGlnLys 645

QY 2101 GCCGAGCCGCAACAACCTTCAGATCAGAGAGCCCTTCCTGGCAAGGCGTGTGTGCCGGAG 2160
Db 646 AlalPProhIsanLeuGlnLeIthAlaAlaPheLeuAlaGlyLeuLeuSerGlnGln 665
QY 2161 CACTGGGGGCGCTGGCTGAGTGGCAAGACATCTGAGAAAGCCCTGCTCCGGAGCCAGCC 2220
Db 666 HisArgAspLeuLeuAlaAlaCysGlnValSerGlnArgValLeuLeuGlnArgGlnAla 685
QY 2221 TGTGCCCGCTGTGTCTGGCCCGAGCCCTCCGCAAGACATTCACATCCCGCCAGCT 2280
Db 686 ArgAlaArgSerCysLeuAlaHisSerLeuArgGlnHisSerIleProAla 705
QY 2281 GCAACGGGTGAGGCAAGCCGCTGACATGCCAGGGGTTCATCTGGGCTACCCGAGC 2340
Db 706 ValProGlnGlnThrLysSerPheHisAlaMetProGlnPheIleThrLeuIleArgSer 725
QY 2341 CTGTACAGATGCAAGAGAGAGGCGCTGGCTCGAAGGCTGCACGCTGGCTGAAGTTGG 2400
Db 726 LeuTyrGlnMetGlnGlnGlnLeuAlaGlnGlnAlaValArgArgLeuAspIleGly 745
QY 2401 CACCTCAAGTTGACATTTGCAAGTGTGGCCGCCACTGAGTGTGCTGGCCTGGCCTTGTG 2460
Db 746 HisLeuLysLeuThrPheCysArgValGlyProAlaGlnCysAlaAlaLeuAlaPheVal 765
QY 2461 CTGACGACCTCCGGCGCCCGCTGGCCCTGCAAGCTGAAGTACAACTCTGTGGTGAATT 2520
Db 766 LeuGlnHisLeuGlnArgProValAlaLeuGlnLeuAspTyrAsnSerValGlyAspVal 785
QY 2521 GGCGTGAAGAGCTGGCTGGCTGGCTGGCTGGCTGGCAAGGCTGTATTGGCGGATAAC 2580
Db 786 GlnValGlnGlnLeuArgProCysLeuGlnValCysThrAlaLeuTyrLeuArgAspAsn 805
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Db 806 AsnIleSerAspArgGlyAlaArgThrLeuValGlnCysAlaLeuArgCysGlnGlnLeu 825
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QY 2701 CTCCCTGCATGCAAGCAGAACTTCTTGCAATTGAGGCTGGGGAAATACTACATCAGTGC 2760
Db 846 LeuLeuAlaHisLysGlnAsnPheLeuSerLeuArgValGlnAsnAsnHisIleThrAla 865
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Db 886 PheIleProGlnAsnSerValGlyAspLysGlyThrGlnAlaLeuAlaGlnValAlaAsp 905
QY 2881 CACCAAGGCTGAAGTGGCTCAAGCTGGTGGGGAACAACATTGGCAAGTGGGTGCCCA 2940
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QY 3121 GCCCTGAAAGAAATGACACCATCTGGAAAGTCTGGCTCCGAGGAAACAATTCTCTTA 3180
Db 986 AlaLeuSerArgAsnSerAlaIleLeuGlnValThrPheLeuArgGlnAsnThrPheSerLeu 1005
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Db 1006 GlnGlnIleGlnThrLeuSerSerArgAspAlaArgLeuLeu 1020

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